



99 2835 54.6 1036 8 ADE37729 Human sec  
100 2835 54.6 1036 8 ADE37613 Human sec

ALIGNMENTS

RESULT 1  
AAB19591  
ID AAB19591 standard; protein; 1055 AA.

XX AC AAB19591;  
XX AC AAB19591;  
DT 22-JAN-2001 (first entry)  
XX DE Human CASB616.

CASB616; EPHB2; ERK; EPH3; EPH3; EPH3; DRT; HEK5; EPHB2v;  
XX KW receptor protein tyrosine kinase; human; antigen; colon cancer;  
XX KW ovary cancer; autoimmune disease; vaccine; therapy; diagnosis.

XX OS Homo sapiens.  
XX PN WO200053216-A2.  
XX PD 14-SEP-2000.

XX PF 28-FEB-2000; 2000WO-EP001587.

XX PR 05-MAR-1999; 99GB-00005124.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX FI Vinals Y De BassolsC;

XX DR WPI; 2000-587384/55.

XX DR N-PSDB; AAA88549.

XX XX Vaccine composition for treating ovarian and colon cancer, comprises  
XX PT CASB616 polypeptides, polynucleotides or antigen presenting cells  
XX PT expressing the polypeptides.

XX PS Claim 1; Page 42; 57pp; English.

XX CC The present sequence is that of human CASB616, a member of the EPH and  
XX CC EPH-related family of receptor protein tyrosine kinases. CASB616 is also  
XX CC known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and EPHB2v. CASB616  
XX CC polypeptides and polynucleotides are important immunogens for specific  
XX CC prophylactic or therapeutic immunization against tumours, especially  
XX CC colon cancer (claimed) and ovarian cancer. They are specifically  
XX CC expressed or highly over-expressed in tumours compared to normal cells  
XX CC and can thus be targeted by antigen-specific immune mechanisms leading to  
XX CC destruction of the tumour cells. They can also be used to diagnose the  
XX CC occurrence of tumour cells. Their inappropriate expression can also cause  
XX CC an induction of autoimmune responses, which can be corrected through  
XX CC vaccination using the CASB616 polypeptides or polynucleotides

XX SQ Sequence 1055 AA;

Query Match 99.9%; Score 5181; DB 3; Length 1055;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRLGALLLLPLLAARETLLMDSTTATLGLWVHPSPGSEVSGYDENMTITYQ 60  
DB 1 MALRLGALLLLPLLAARETLLMDSTTATLGLWVHPSPGSEVSGYDENMTITYQ 60  
QY 61 VCNVFESSQNNWLRTKFIIRRGARHRIHVEMKFSVRDCSSIPSPGCKETFNLYYEADF 120  
DB 61 VCNVFESSQNNWLRTKFIIRRGARHRIHVEMKFSVRDCSSIPSPGCKETFNLYYEADF 120  
QY 121 DSATKTFPNWENPWVKVDTTAADESFSQVLDLGRVWVKINTEVRSFGPVSRSFYLAFO 180

DB 121 DSATKTFPNWENPWVKVDTTAADESFSQVLDLGRVWVKINTEVRSFGPVSRSFYLAFO 180  
QY 181 YGCMSLIAVRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
DB 181 YGCMSLIAVRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
QY 241 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTGTFKANQGDCACTHCPINSRTTSEGA 300  
DB 241 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTGTFKANQGDCACTHCPINSRTTSEGA 300  
QY 301 TNCVCRNGYRADLDPLDMPCTTIPSAQAIVSSVNETSLMLEWTPPRSGGREDILVYNI 360  
DB 301 TNCVCRNGYRADLDPLDMPCTTIPSAQAIVSSVNETSLMLEWTPPRSGGREDILVYNI 360  
QY 361 ICKSCGSRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGVTQSPF 420  
DB 361 ICKSCGSRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGVTQSPF 420  
QY 421 SPOFASVNITTNOAAPSASVIMHQVSRVTDSITLSWSQDPQNGVILDYELQYKEKELSE 480  
DB 421 SPOFASVNITTNOAAPSASVIMHQVSRVTDSITLSWSQDPQNGVILDYELQYKEKELSE 480  
QY 481 YNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTTEAEYQTSIOEK 540  
DB 481 YNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTTEAEYQTSIOEK 540  
QY 541 LPLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600  
DB 541 LPLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600  
QY 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660  
DB 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660  
QY 661 EKORDFLSEASIMGQFDHPNVTHLEGVTKSTPVMIIITEFMENGSLDSFLRNDGQFTV 720  
DB 661 EKORDFLSEASIMGQFDHPNVTHLEGVTKSTPVMIIITEFMENGSLDSFLRNDGQFTV 720  
QY 721 IQLVGMRLGIAAGMKYLADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPTY 780  
DB 721 IQLVGMRLGIAAGMKYLADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPTY 780  
QY 781 TSALGCKIPIRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWMTNQDVINAIE 840  
DB 781 TSALGCKIPIRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWMTNQDVINAIE 840  
QY 841 QDYRLPPMDPCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSGI 900  
DB 841 QDYRLPPMDPCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSGI 900  
QY 901 NLPLDRTIPDYTSFNTVDEWLEAIIKMGQYKESFANAGTSTFDVVSQMMEDILRIGVTL 960  
DB 901 NLPLDRTIPDYTSFNTVDEWLEAIIKMGQYKESFANAGTSTFDVVSQMMEDILRIGVTL 960  
QY 961 AGHOKKILNSIQWRAQMNQIQSVE 985  
DB 961 AGHOKKILNSIQWRAQMNQIQSVE 985

RESULT 2  
ABU07847  
ID ABU07847 standard; protein; 1055 AA.

XX AC ABU07847;  
XX AC ABU07847;  
DT 10-MAY-2003 (first entry)

XX DE Human ephrin receptor ligand EphB2.

XX KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;  
XX KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;  
XX KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;  
XX KW cell migration disorder; cell proliferation disorder; neovascularisation;

KW ischaemia; infarction; tissue graft; transplanted; human;  
KW ephrin receptor ligand; tie receptor tyrosine kinase; EphB2.

OS Homo sapiens.

PN W02003004529-A2.

XX 16-JAN-2003.

XX 02-JUL-2002; 2002WO-IB002524.

XX 02-JUL-2001; 2001US-0302960P.

XX (LICN ) LICENTIA LTD.

XX Alitalo K, Kubo H;

XX WPI; 2003-210341/20.

XX N-PSDB; ABX12548.

XX Identifying modulators of binding between a Tie receptor tyrosine kinase  
PT and an Ephrin ligand, useful for promoting neovascularization, comprises  
PT contacting a Tie receptor with an Ephrin in the presence of a putative  
PT modulator.

XX Disclosure; Page 128-132; 199pp; English.

XX The invention describes a method of identifying a modulator of binding  
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method  
CC comprises contacting a Tie receptor composition with an Ephrin  
CC composition in the presence and in the absence of a putative modulator  
CC compound, and detecting the binding between the Tie receptor and the Ephrin  
CC in the presence and in the absence of the putative modulator. The method  
CC is useful for identifying a modulator of binding between a Tie receptor  
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the  
CC method are useful in modulating angiogenic processes, including  
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-  
CC Tie biology, aberrant growth, migration or proliferation of cells that  
CC express a Tie receptor, or for promoting growth of vessel or  
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or  
CC chronic compound, or a tissue graft or transplant). This is the amino  
CC acid sequence of human EphB2, a member of the Ephrin-B subclass of  
CC ligands that are bound to the membrane via a transmembrane domain and  
CC short cytoplasmic tail and function as Ephrin receptor ligands

XX Sequence 1055 AA;

Query Match 99.98; Score 5181; DB 6; Length 1055;  
Best Local Similarity 99.98; Pred. No. 0;  
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRLLGALLLLPLLAAVEETLMDSTATAELGMMVHPSPGVEVSGYDENMNTIRTYQ 60  
DB 1 MALRRLLGALLLLPLLAAVEETLMDSTATAELGMMVHPSPGVEVSGYDENMNTIRTYQ 60  
QY 61 VCNVFESSQNWLRTKFIERRGAHRIHVMKFSVRDCSSIPSPGCKETFNLYYYEADF 120  
DB 61 VCNVFESSQNWLRTKFIERRGAHRIHVMKFSVRDCSSIPSPGCKETFNLYYYEADF 120  
QY 121 DSATKTFPNMWNPNWVKVDITIADESQVDLGGRVNKMINTVRSFGVSRSGFYLAQD 180  
DB 121 DSATKTFPNMWNPNWVKVDITIADESQVDLGGRVNKMINTVRSFGVSRSGFYLAQD 180  
QY 181 YGGCMSLIAVRFVRKCPRIIONCAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
DB 181 YGGCMSLIAVRFVRKCPRIIONCAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
QY 241 CNGDGEWLVPICRCMKAGFEAVENGTVCRGCPSTGTFKANQGDCACTHCPINRSTTSEGA 300  
DB 241 CNGDGEWLVPICRCMKAGFEAVENGTVCRGCPSTGTFKANQGDCACTHCPINRSTTSEGA 300  
QY 301 TNCVCRNGYYRADLDPDLMCTTIPSAQVAIVSSVNETSLMLEWTPPRDSSGGREDLYNI 360

DB 301 TNCVCRNGYYRADLDPDLMCTTIPSAQVAIVSSVNETSLMLEWTPPRDSSGGREDLYNI 360  
QY 361 ICKSCSGRGACTRCGDNVQYAPRQLGLTEPRYIYISDLAHTQYTFEIQAVNGVTDQSPF 420  
DB 361 ICKSCSGRGACTRCGDNVQYAPRQLGLTEPRYIYISDLAHTQYTFEIQAVNGVTDQSPF 420  
QY 421 SPOFASVNTTNOAAPSASVIMHQVSRVTDSITLSWSQDPQPNQGVILDELYQYKEKELSE 480  
DB 421 SPOFASVNTTNOAAPSASVIMHQVSRVTDSITLSWSQDPQPNQGVILDELYQYKEKELSE 480  
QY 481 YNATAIKSPNTNTVVOGLKAGAIYVQVRARTVAGYGRYSGKMYFQMTAEAYTSIQEK 540  
DB 481 YNATAIKSPNTNTVVOGLKAGAIYVQVRARTVAGYGRYSGKMYFQMTAEAYTSIQEK 540  
QY 541 LPLIIGSSAAGLVFLIAVAVIAIVCNRRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPF 600  
DB 541 LPLIIGSSAAGLVFLIAVAVIAIVCNRRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPF 600  
QY 601 TYEDPNEAVREPAKEIDISCVKIEQVIGAGEFGEVCSGHUKLPGRKRIFVAIKTLKSGYT 660  
DB 601 TYEDPNEAVREPAKEIDISCVKIEQVIGAGEFGEVCSGHUKLPGRKRIFVAIKTLKSGYT 660  
QY 661 EKORRDFLSEASIMGQFDHENVHLEGVVTKSTPVMIIITEFMENGSLDLSFLRQNDGQFTV 720  
DB 661 EKORRDFLSEASIMGQFDHENVHLEGVVTKSTPVMIIITEFMENGSLDLSFLRQNDGQFTV 720  
QY 721 IQLVGLMRLGIAAGMKYLADNMVYVHRDLAARNILVNSNLVCKVSDFGLSRLEDDTSDPT 780  
DB 721 IQLVGLMRLGIAAGMKYLADNMVYVHRDLAARNILVNSNLVCKVSDFGLSRLEDDTSDPT 780  
QY 781 TSALGKIPIRWTAPBAIQVRKTSASDVMSYGIWMEVMSYGERPFWDMTNQDVINAIE 840  
DB 781 TSALGKIPIRWTAPBAIQVRKTSASDVMSYGIWMEVMSYGERPFWDMTNQDVINAIE 840  
QY 841 QDYRLPPMDPCPSALHQLMDCWQKORNRHPRKFGQIVNTLDMIRNPNLSKAMAPLSSGI 900  
DB 841 QDYRLPPMDPCPSALHQLMDCWQKORNRHPRKFGQIVNTLDMIRNPNLSKAMAPLSSGI 900  
QY 901 NLPLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTL 960  
DB 901 NLPLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTL 960  
QY 961 AGHQKILNSIQVMRAQMNQIQSVE 985  
DB 961 AGHQKILNSIQVMRAQMNQIQSVE 985

RESULT 3  
ADL61215  
ID ADL61215 standard; protein; 1055 AA.  
XX  
AC ADL61215;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human protein tyrosine kinase biomarker EphB2 protein.  
XX  
KW predictor set; protein tyrosine kinase; cytostatic; antiangiogenic;  
KW vasotrophic; vulnary; pharmacogenomic; drug sensitivity; breast cancer;  
KW hypervascular disease; angiogenesis; wound healing scar; human;  
XX biomarker; EphB2.  
OS Homo sapiens.  
XX  
XX WO2004020583-A2.  
XX  
PD 11-MAR-2004.  
XX  
XX 26-AUG-2003; 2003WO-US026491.  
XX  
PR 27-AUG-2002; 2002US-0406385P.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Huang F, Han X, Reeves KA, Amler L, Fairchild CR, Lee FY;  
PI Shaw P;  
XX WPI; 2004-239171/22.  
DR N-PSDB; ADL61078.  
XX New predictor sets with a plurality of polynucleotides and/or  
PT polypeptides whose expression pattern predicts cell response to a  
PT compound that modulates protein tyrosine kinase activity, useful in  
PT treating breast cancer.  
XX Claim 9; SEQ ID NO 139; 649pp; English.  
XX The invention relates to a novel predictor set comprising a plurality of  
CC polynucleotides and/or polypeptides whose expression pattern is  
CC predictive of the response of cells to treatment with a compound that  
CC modulates protein tyrosine kinase activity or members of the protein  
CC tyrosine kinase pathway. The molecules of the invention demonstrate  
CC cytosolic, antiangiogenic, vasotrophic and vulnerary activities and may  
CC be useful in the field of pharmacogenomics, in particular for determining  
CC drug sensitivity and in treating breast cancer, hypervascular diseases, of  
CC angiogenesis and scars in wound healing. The current sequence is that of  
CC a human protein tyrosine kinase biomarker protein of the invention.  
XX  
XX  
SQ Sequence 1055 AA;

Query Match 99.9%; Score 5181; DB 8; Length 1055;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRLGAALLLLPAAVEETLMDSTTAAELGMMVHPSPGWEVSGYDENMTIYQ 60  
Db 1 MALRLGAALLLLPAAVEETLMDSTTAAELGMMVHPSPGWEVSGYDENMTIYQ 60  
Qy 61 VCNVFESSQNNWLRTKPIRRGAHRIHVMKFSVRDCSSIPSPGCKETFNLYYBDF 120  
Db 61 VCNVFESSQNNWLRTKPIRRGAHRIHVMKFSVRDCSSIPSPGCKETFNLYYBDF 120  
Qy 121 DSATKTPNNMENPWKVDTTAADESFSQVLDGRVMKINTEVRSFGVPSRSGYLAQD 180  
Db 121 DSATKTPNNMENPWKVDTTAADESFSQVLDGRVMKINTEVRSFGVPSRSGYLAQD 180  
Qy 181 YGGCMLIAVAVFYRKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
Db 181 YGGCMLIAVAVFYRKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
Qy 241 CNGDGEMLVPIGRMCCKAGFAVENGTVCRCGPGSTFKANQGDCACTHCPINSRTTSEGA 300  
Db 241 CNGDGEMLVPIGRMCCKAGFAVENGTVCRCGPGSTFKANQGDCACTHCPINSRTTSEGA 300  
Qy 301 TNCVCRNGYYRADLDPLDMPCTTIPSAQAVISSVNETSLMELWTPPRDSCGREDLVNI 360  
Db 301 TNCVCRNGYYRADLDPLDMPCTTIPSAQAVISSVNETSLMELWTPPRDSCGREDLVNI 360  
Qy 361 CKSCGSRGACTRCGDNVOYAPRQLGLTEPRIVISDLAHTQYTFEIQAVNGVTDQSPF 420  
Db 361 CKSCGSRGACTRCGDNVOYAPRQLGLTEPRIVISDLAHTQYTFEIQAVNGVTDQSPF 420  
Qy 421 SPQFASVNTTNOAPSASVIMHVSRTVDSITLSWSPDQPNQVILDYELQYKEKELSE 480  
Db 421 SPQFASVNTTNOAPSASVIMHVSRTVDSITLSWSPDQPNQVILDYELQYKEKELSE 480  
Qy 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMFQWTEAEYQTSIQEK 540  
Db 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMFQWTEAEYQTSIQEK 540  
Qy 541 LPLIIGSSAAGLVFLIAVWVIAVCNRRGFPRADSEYTDKLOHTYSGHMTPGMKIYIDPF 600  
Db 541 LPLIIGSSAAGLVFLIAVWVIAVCNRRGFPRADSEYTDKLOHTYSGHMTPGMKIYIDPF 600  
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYT 660  
Db 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYT 660

Db 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGYT 660  
Qy 661 EKORDFLSEASIMGQFHPNVIHLEGGVTKSTPMWITTEFMENGLSDSFLRQNDGQFTV 720  
Db 661 EKORDFLSEASIMGQFHPNVIHLEGGVTKSTPMWITTEFMENGLSDSFLRQNDGQFTV 720  
Qy 721 IQLVGMRLGIAAGMKYLADNMVYVHRDLAARNILVNSLVCKVSDFLSFLSDEDDTSDPTY 780  
Db 721 IQLVGMRLGIAAGMKYLADNMVYVHRDLAARNILVNSLVCKVSDFLSFLSDEDDTSDPTY 780  
Qy 781 TSALGKIPIRWTAPETAIQYRKFTSASDVWSVGIWVWEVMSYGERPYWMTNQDVINAIE 840  
Db 781 TSALGKIPIRWTAPETAIQYRKFTSASDVWSVGIWVWEVMSYGERPYWMTNQDVINAIE 840  
Qy 841 QYRLPPPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKWRNPNLSLKAMAPLSSGI 900  
Db 841 QYRLPPPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKWRNPNLSLKAMAPLSSGI 900  
Qy 901 NLPLDRTTIPDYTSFNTVDWELEAIKMGQYKESFANAGTSTFDVVSQMMEDILRLGVTL 960  
Db 901 NLPLDRTTIPDYTSFNTVDWELEAIKMGQYKESFANAGTSTFDVVSQMMEDILRLGVTL 960  
Qy 961 AGHQKILNSIQVMRAQMNQIOSVE 985  
Db 961 AGHQKILNSIQVMRAQMNQIOSVE 985

RESULT 4  
AAB19590  
ID AAB19590 standard; protein; 987 AA.  
XX  
AC AAB19590;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Human CASB616.  
XX  
KW CASB616; EPB2; ERK; EPB3; EPHT3; DRT; HRK5; EPB2v;  
KW receptor protein tyrosine kinase; human; antigen; colon cancer;  
KW ovary cancer; tumour; autoimmune disease; vaccine; therapy; diagnosis.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 568..569  
FT /note= "an additional Arg residue decodes from the  
FT CASB616 nucleotide sequence given in the specification  
FT (see AAA88548), but is not given in the CASB616 amino  
FT acid sequence in the specification"  
FT Misc-difference 956  
FT /note= "encoded by GTT"  
XX  
XX WC200053216-A2.  
XX  
XX 14-SEP-2000.  
XX  
XX 28-FEB-2000; 2000WO-EP001587.  
XX  
XX 05-MAR-1999; 99GB-00005124.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX Vinals Y De BaesoleC;  
XX  
XX WPI; 2000-587384/55.  
XX  
XX N-PSDB; AAA88548.  
XX  
XX Vaccine composition for treating ovarian and colon cancer, comprises  
XX CASB616 polypeptides, polynucleotides or antigen presenting cells  
XX expressing the polypeptides.  
XX  
XX Claim 1; Page 41; 57pp; English.



CC The present sequence is that of human CASB616, a member of the EPH and  
CC EPH-related family of receptor protein tyrosine kinases. CASB616 is also  
CC known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and EPHB2v. CASB616  
CC polypeptides and polynucleotides are important immunogens for specific  
CC prophylactic or therapeutic immunization against tumours, especially  
CC colon cancer (claimed) and ovarian cancer. They are specifically  
CC expressed or highly over-expressed in tumours compared to normal cells  
CC and can thus be targeted by antigen-specific immune mechanisms leading to  
CC destruction of the tumour cells. They can also be used to diagnose the  
CC occurrence of tumour cells. Their inappropriate expression can also cause  
CC an induction of autoimmune responses, which can be corrected through  
CC vaccination using the CASB616 polypeptides or polynucleotides  
XX  
SQ Sequence 987 AA;

Query Match 99.8%; Score 5177.5; DB 3; Length 987;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 986; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MALRRGAALLLLPAAVEETLMDSTTATAELGMMVHPSPSGVEVSGYDENMTIRTYQ 60  
Db 1 MALRRGAALLLLPAAVEETLMDSTTATAELGMMVHPSPSGVEVSGYDENMTIRTYQ 60

Qy 61 VCNVFESSQNNWLRKTIIRRGARHIVEMKFSVRDCSSIPSPVSGCKETFNLYYEADF 120  
Db 61 VCNVFESSQNNWLRKTIIRRGARHIVEMKFSVRDCSSIPSPVSGCKETFNLYYEADF 120

Qy 121 DSATKTPNNMENPWKVDVTTAADESPQDLGRVWKINTEVSPGVSRSGLYLAQD 180  
Db 121 DSATKTPNNMENPWKVDVTTAADESPQDLGRVWKINTEVSPGVSRSGLYLAQD 180

Qy 181 YGGCMSLIAVRFYRKCPRIITQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
Db 181 YGGCMSLIAVRFYRKCPRIITQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240

Qy 241 CNGDGEMLVPTGRCMWCKAGFAVNGTVCRGCPSTFKANQGDCACTHCPINSRTTSEGA 300  
Db 241 CNGDGEMLVPTGRCMWCKAGFAVNGTVCRGCPSTFKANQGDCACTHCPINSRTTSEGA 300

Qy 301 TNCVCRNGYRADLDLDMPCCTTIPSAQVAIVSSNETSLMWTTPRDSGREDLYVNI 360  
Db 301 TNCVCRNGYRADLDLDMPCCTTIPSAQVAIVSSNETSLMWTTPRDSGREDLYVNI 360

Qy 361 ICKSCGSGRGAACRGDNVQAPQLGLTEPRIVISDLAHTQYTFEIQAVNGVTDOSPF 420  
Db 361 ICKSCGSGRGAACRGDNVQAPQLGLTEPRIVISDLAHTQYTFEIQAVNGVTDOSPF 420

Qy 421 SPQFASVNTTNOAAPSASVIMHQSRTVDSITLSWSQDPQNGVILDYELQYKEKELSE 480  
Db 421 SPQFASVNTTNOAAPSASVIMHQSRTVDSITLSWSQDPQNGVILDYELQYKEKELSE 480

Qy 481 YNATAIKSPNTVTVOGLKAGAVVFOVARTVAGYGRYSKMYFQMTTEAEYQTSIOEK 540  
Db 481 YNATAIKSPNTVTVOGLKAGAVVFOVARTVAGYGRYSKMYFQMTTEAEYQTSIOEK 540

Qy 541 LPLIIGSSAAGLVFLIAVWVIAVCN-RRGFERADSEYTDKLOHYTSGHMTPGMKIYIDP 599  
Db 541 LPLIIGSSAAGLVFLIAVWVIAVCNRRRGERADSEYTDKLOHYTSGHMTPGMKIYIDP 600

Qy 600 FTYEDPNEAVREFAKEIDISCKIEQVIGAGEFECVSGHKLPGKREIFVAIKLKSQY 659  
Db 601 FTYEDPNEAVREFAKEIDISCKIEQVIGAGEFECVSGHKLPGKREIFVAIKLKSQY 660

Qy 660 TEKORRDLFSLASIMGQDPHNVTHLEGVTKSTFVMIITFEFMENGLSDSLRQNDQFT 719  
Db 661 TEKORRDLFSLASIMGQDPHNVTHLEGVTKSTFVMIITFEFMENGLSDSLRQNDQFT 720

Qy 720 VIQLVGLMRGTAAGWKYLDMMVYHRLAARNILVNSNLCKVSDFDGLSFLRQDSDPT 779  
Db 721 VIQLVGLMRGTAAGWKYLDMMVYHRLAARNILVNSNLCKVSDFDGLSFLRQDSDPT 780

Qy 780 YTSALGGKIPIRWTAPEAIQYRKFTSADSWSYGIVMVEVMSYGERPYWDMTNDQVINAI 839  
XX

Db 781 YTSALGGKIPIRWTAPEAIQYRKFTSADSWSYGIVMVEVMSYGERPYWDMTNDQVINAI 840  
Qy 840 EQDYRLPPPPDCPSALHQLMDCWQKDNHRPKFGQIVNTLDKMRPNPSLKAWAPLSSG 899  
Db 841 EQDYRLPPPPDCPSALHQLMDCWQKDNHRPKFGQIVNTLDKMRPNPSLKAWAPLSSG 900  
Qy 900 INLPDLLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFQVVSQMMEDILRLGVT 959  
Db 901 INLPDLLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFQVVSQMMEDILRLGVT 960

Qy 960 LAGHOKKIILNSIQVMRAQMNQIQSV 986  
Db 961 LAGHOKKIILNSIQVMRAQMNQIQSV 987

RESULT 5  
ADN39875  
ID ADN39875 standard; protein; 987 AA.

XX AC ADN39875;  
XX DT 17-JUN-2004 (first entry)  
XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C245.  
XX Human; differential expression; cancer; angiogenic disorder;  
XX fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
XX inflammatory disease; autoimmune disease;  
XX retinal neovascularisation syndrome; scarring; uterine fibroid;  
XX detection; diagnosis; prognosis; drug screening; drug targeting;  
XX wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
XX vulneryary; gene therapy; vaccine.  
XX Homo sapiens.  
XX WO2003042661-A2.  
XX 22-MAY-2003.  
XX 13-NOV-2002; 2002WO-US036810.  
XX 13-NOV-2001; 2001US-0350666P.  
XX 21-NOV-2001; 2001US-0332464P.  
XX 29-NOV-2001; 2001US-0334393P.  
XX 03-DEC-2001; 2001US-0335394P.  
XX 14-DEC-2001; 2001US-0340376P.  
XX 08-JAN-2002; 2002US-0347211P.  
XX 10-JAN-2002; 2002US-0347349P.  
XX 08-FEB-2002; 2002US-0355250P.  
XX 13-FEB-2002; 2002US-0356714P.  
XX 20-FEB-2002; 2002US-0359077P.  
XX 29-MAR-2002; 2002US-0368809P.  
XX 04-APR-2002; 2002US-0370110P.  
XX 12-APR-2002; 2002US-0372466P.  
XX 05-JUN-2002; 2002US-0386614P.  
XX 16-JUL-2002; 2002US-0396839P.  
XX 22-JUL-2002; 2002US-0397775P.  
XX 22-JUL-2002; 2002US-0397845P.  
XX 09-SEP-2002; 2002US-0409450P.  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
XX Afar D, Aziz N, Gineburg WM, Gish KC, Glynn R, Hevezi PA;  
XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
XX WPI; 2003-468649/44.  
XX N-PSDB; ADN39858.  
XX Determining the presence or absence of a pathological cell in a patient,  
XX useful for diagnosing, prognosing or treating cancer, comprises detecting  
XX a nucleic acid in a biological sample.  
XX Claim 12; SEQ ID NO C245; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
 CC whose expression is upregulated or downregulated in specific cancers or  
 CC other diseases such as angiogenic or fibrotic disorders, and to methods  
 CC of determining the presence or absence of a pathological cell in a  
 CC patient by detecting a nucleic acid at least 80% identical to those of  
 CC the invention or by detecting a polypeptide of the invention. The  
 CC invention also relates to expression vectors and host cells comprising a  
 CC nucleic acid of the invention; antibodies which specifically bind a  
 CC polypeptide of the invention; use of such antibodies for drug targeting;  
 CC and methods of screening for modulators of activity or expression of the  
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
 CC antibodies and methods are useful for diagnosing, prognosing and treating  
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
 CC neovascularisation syndromes, scarring and uterine fibroids. They may  
 CC also be useful in wound healing and in contraception. The present  
 CC sequence represents a polypeptide of the invention.  
 XX  
 SQ Sequence 987 AA;

Query Match 99.7%; Score 5171.5; DB 7; Length 987;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 984; Conservative 2; Mismatches 0; Indels 1; Gaps 1;  
 1 MALRRLLGAALLLLPLLAAVETLMDSTTATAELGMMVHPSPGWEVSGYDENMTTIRTYQ 60  
 1 MALRRLLGAALLLLPLLAAVETLMDSTTATAELGMMVHPSPGWEVSGYDENMTTIRTYQ 60  
 61 VCNVFESSQNNLRTKFIERRGAHRIHVMKFSVRDCSSIPSPGCKETFNLYYBADF 120  
 61 VCNVFESSQNNLRTKFIERRGAHRIHVMKFSVRDCSSIPSPGCKETFNLYYBADF 120  
 121 DSATKTFPNMENPWKVDITIADESQVDLGRVVKINTEVRSPGVSRSFYLAQD 180  
 121 DSATKTFPNMENPWKVDITIADESQVDLGRVVKINTEVRSPGVSRSFYLAQD 180  
 181 YGGCMLIAVRFYRKPRIIIONGAIQFETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
 181 YGGCMLIAVRFYRKPRIIIONGAIQFETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
 241 CNGDEWLVPITGRCMCKAGFEAVENGTCRGCPSTFKANQGDACHTCPINSRTTSEGA 300  
 241 CNGDEWLVPITGRCMCKAGFEAVENGTCRGCPSTFKANQGDACHTCPINSRTTSEGA 300  
 301 TNCVCRNGYRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPRDSGGREDLYVNI 360  
 301 TNCVCRNGYRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPRDSGGREDLYVNI 360  
 361 CKSCGSGRGACTRCGNVQVAPRQLGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPF 420  
 361 CKSCGSGRGACTRCGNVQVAPRQLGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPF 420  
 421 SPQFASVNTTNOAPSASVIMHQVSRVDSITLSWSQPPQNGVILDYELQYKEKELSE 480  
 421 SPQFASVNTTNOAPSASVIMHQVSRVDSITLSWSQPPQNGVILDYELQYKEKELSE 480  
 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540  
 481 YNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEK 540  
 541 LPLIIGSSAAGLVFLIAVWVIAVCN-RRGERADSEYTDKLOHYTSGHMTPGMKIYIDP 599  
 541 LPLIIGSSAAGLVFLIAVWVIAVCNRRRGERADSEYTDKLOHYTSGHMTPGMKIYIDP 600  
 600 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAKITLKSQY 659  
 601 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAKITLKSQY 660  
 660 TEKORRFLSEASIMGQFDHNVHLEGVVTKSPVMILTEFMENGSLDSFLRQNDGQFT 719  
 661 TEKORRFLSEASIMGQFDHNVHLEGVVTKSPVMILTEFMENGSLDSFLRQNDGQFT 720

QY 720 VIQVGMRLGIAAGMKYLADNMVYHRDLAARNILVNSNLVCKVSDFGLSRLEDDTSDPT 779  
 DB 721 VIQVGMRLGIAAGMKYLADNMVYHRDLAARNILVNSNLVCKVSDFGLSRLEDDTSDPT 780  
 QY 780 YTSALGKGIPIRWTAPEAIQYRKFTSASDVWSYGIWVWEVMSYGERPYWDMTQDVINAI 839  
 DB 781 YTSALGKGIPIRWTAPEAIQYRKFTSASDVWSYGIWVWEVMSYGERPYWDMTQDVINAI 840  
 QY 840 EQYRLPPPMDCPSALHQLMDCQKDRHPRKFGQIVNTLDKWIENPNSLKAWAPLSSG 899  
 DB 841 EQYRLPPPMDCPSALHQLMDCQKDRHPRKFGQIVNTLDKWIENPNSLKAWAPLSSG 900  
 QY 900 INLPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVVSQMMEDILRLGVT 959  
 DB 901 INLPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVVSQMMEDILRLGVT 960  
 QY 960 LAGHQKKILNSIQVMRAQMNQIOSVEV 986  
 DB 961 LAGHQKKILNSIQVMRAQMNQIOSVEV 987  
 RESULT 6  
 AAW26366  
 ID AAW26366 standard; protein; 994 AA.  
 XX AC AAW26366;  
 XX AC AAW26366;  
 DT 02-DEC-1997 (first entry)  
 XX Mouse Nuk tyrosine kinase.  
 DE DE  
 XX Nuk tyrosine kinase.  
 KW Nuk tyrosine kinase; Eph receptor tyrosine kinase; signal transduction;  
 KW axonogenesis; neurodegenerative disease; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; multiple sclerosis;  
 KW amyotrophic lateral sclerosis; Wernicke's disease; nerve damage; trauma;  
 KW ischaemia; stroke.  
 XX OS Mus musculus.  
 XX PH Location/Qualifiers  
 FT Peptide 1..26  
 FT Protein /label= Sig\_peptide  
 FT Domain /label= Mat\_protein  
 FT Region 27..548  
 FT Region /label= Extracellular\_domain  
 FT Region 330..420  
 FT Region /note= FNIII  
 FT Region 444..534  
 FT Region /label= FNIII  
 FT Domain /note= "fibronectin type III repeat"  
 FT Domain 549..574  
 FT Domain /label= Transmembrane\_domain  
 FT Domain 575..994  
 FT Region /label= Cytoplasmic\_domain  
 FT Region 623..888  
 FT Region /label= Tyrosine-kinase\_region  
 XX WO9714966-A1.  
 XX 24-APR-1997.  
 XX 10-OCT-1996; 96WO-CA000679.  
 XX 13-OCT-1995; 95US-0005518P.  
 XX (MOUN ) MOUNT SINAI HOSPITAL CORP.  
 XX Pawson A, Henkemeyer M;  
 XX WPI; 1997-245245/22.  
 DR N-PSDB; AAT84528.

XX Activation of ligand regulatory pathways by Eph subfamily receptor  
 PT tyrosine kinases - for stimulating or inhibiting axonogenesis, useful for  
 PT treatment of e.g. neurodegenerative diseases such as Alzheimer's or  
 PT Parkinson's diseases.  
 XX Disclosure; Fig 3; 55pp; English.  
 XX  
 XX Murine Nuk tyrosine kinase is an Eph subfamily receptor tyrosine kinase  
 CC that is essential for formation of the medial tract of the anterior  
 CC commissure of the brain, and which appears to play a role in the  
 CC formation of the habenular interpeduncular tract. Its amino acid sequence  
 CC was deduced from cDNA clones (see AAR84528) isolated from an embryo cDNA  
 CC library. The extracellular domain of Nuk was shown to be sufficient for  
 CC formation of the medial tract. Eph subfamily receptor tyrosine kinases  
 CC (e.g. the Nuk extracellular domain) can be used in claimed methods to:  
 CC activate a ligand regulatory pathway in a cell; identify substances able  
 CC to bind a ligand for an Eph subfamily receptor tyrosine kinase; and to  
 CC affect neuronal development or regeneration, especially the stimulation  
 CC or inhibition of axonogenesis, in a mammal. Activation of the ligand  
 CC regulatory pathway results in downstream activation of a series of  
 CC regulatory pathways in cells that control gene expression, cell division,  
 CC cytoskeletal architecture, cell metabolism, cell migration and cell-cell  
 CC interactions. Substances which activate the ligand regulatory pathway may  
 CC be used for stimulating or inhibiting neuronal development regeneration  
 CC and axonal migration associated with neurodegenerative disease e.g.  
 CC Alzheimer's, Parkinson's or Huntington's diseases, multiple sclerosis,  
 CC amyotrophic lateral sclerosis, deficiency diseases such as Wernicke's  
 CC disease, peripheral nerve damage, trauma and ischaemia resulting from  
 CC stroke  
 XX  
 XX Sequence 994 AA;

Query Match 98.9%; Score 5130; DB 2; Length 994;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 10 LLLPLLA AVEETLMDSTTATAELAGMNVHPSPGWEVSGYDENNTTIRTYQVCNVFESSQ 69  
 DB 18 LLLPLLA AVEETLMDSTTATAELAGMNVHPSPGWEVSGYDENNTTIRTYQVCNVFESSQ 77

QY 70 NNWLRTFIRRRGARRHIVEMKFSVRDCSSIPSPGCKETFNLYYEADPDSATKTFPN 129  
 DB 78 NNWLRTFIRRRGARRHIVEMKFSVRDCSSIPSPGCKETFNLYYEADPDLATKTFPN 137

QY 130 WMENPWVKVDITIADESFSQVDLGGRYWKINTEVRSFGPVSRNGFYLAFOYGGCMLIA 189  
 DB 138 WMENPWVKVDITIADESFSQVDLGGRYWKINTEVRSFGPVSRNGFYLAFOYGGCMLIA 197

QY 190 VRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGSEWL 249  
 DB 198 VRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGSEWL 257

QY 250 PIGRCMKAGFEAVENGTVCRGCPSPGTFKANQGDGEACTHCPINSRTTSEGATNCVCNRY 309  
 DB 258 PIGRCMKAGFEAVENGTVCRGCPSPGTFKANQGDGEACTHCPINSRTTSEGATNCVCNRY 317

QY 310 YRADLDPMDPCTTIPAPQAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSCSGR 369  
 DB 318 YRADLDPMDPCTTIPAPQAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSCSGR 377

QY 370 GACTRCGDNQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFPQFASVNI 429  
 DB 378 GACTRCGDNQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFPQFASVNI 437

QY 430 TTNOAPSASVIMHQVSRVDSITLSWQDPQNGVILDYELQYKEKSELYNATAIKSP 489  
 DB 438 TTNOAPSASVIMHQVSRVDSITLSWQDPQNGVILDYELQYKEKSELYNATAIKSP 497

QY 490 TINTVVOGLKAGALYVFOVRARTVAGYGRYSGKMYFQMTAEAYQTSIQSKLPIIGSSA 549  
 DB 498 TINTVVOGLKAGALYVFOVRARTVAGYGRYSGKMYFQMTAEAYQTSIQSKLPIIGSSA 557

QY 550 AGLVFLIAVVIIVAIIVNRRGFERADSEYTDKLOHYTSGHMTGPKIYIDPFTYEDPNEAV 609  
 DB 558 AGLVFLIAVVIIVAIIVNRRGFERADSEYTDKLOHYTSGHMTGPKIYIDPFTYEDPNEAV 617

QY 610 REFAKIDIDSCVKIEQVIGAGEGECVSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLS 669  
 DB 618 REFAKIDIDSCVKIEQVIGAGEGECVSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLS 677

QY 670 EASIMQGFDPHNPVHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVIQLVGMRLG 729  
 DB 678 EASIMQGFDPHNPVHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVIQLVGMRLG 737

QY 730 IAAGMYKILADNMVYVHRDLAARNILVNSNLVCKVDFGLSRFLDEDDTSDPYTSALGQKIP 789  
 DB 738 IAAGMYKILADNMVYVHRDLAARNILVNSNLVCKVDFGLSRFLDEDDTSDPYTSALGQKIP 797

QY 790 IRTAPEAQYRKFTSASDVMSYGIYVMEVMSYGERPYMDMTNQDVINAIEQDYRLPPPM 849  
 DB 798 IRTAPEAQYRKFTSASDVMSYGIYVMEVMSYGERPYMDMTNQDVINAIEQDYRLPPPM 857

QY 850 DCPALHQLMLDCWQKDRNHRPKFGQIVNTLDKMIKNPNSLKAMAPLSSGINLPDLRTI 909  
 DB 858 DCPALHQLMLDCWQKDRNHRPKFGQIVNTLDKMIKNPNSLKAMAPLSSGINLPDLRTI 917

QY 910 PDYTSFNTVDEWLEAIKMGQYKESFANAGTSPDVVSQMMEDILRLGVTLAGHQKILN 969  
 DB 918 PDYTSFNTVDEWLEAIKMGQYKESFANAGTSPDVVSQMMEDILRLGVTLAGHQKILN 977

QY 970 SIQVMAQNMQIOSVEV 986  
 DB 978 SIQVMAQNMQIOSVEV 994

RESULT 7  
 AAU01907  
 ID AAU01907 standard; protein; 994 AA.  
 XX  
 XX AAU01907;  
 XX AC AC  
 XX XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE Murine neural kinase (Nuk) polypeptide.  
 XX  
 KW Neural kinase; Nuk; receptor tyrosine kinase; axonal migration; stroke;  
 KW nerve fibre; cell-cell interaction; axonogenesis; neuronal development;  
 KW regeneration; neurodegenerative disorder; Alzheimer's disease; ischaemia;  
 KW Parkinson's disease; Huntington's disease; demyelinating disease;  
 KW multiple sclerosis; amyotrophic lateral sclerosis; deficiency disease;  
 KW Wernicke's disease; nutritional polyneuropathy; multistep degeneration;  
 KW progressive supranuclear palsy; Shy Drager's syndrome; mouse;  
 KW olivoponto cerebellar atrophy; peripheral nerve damage.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT Domain /note= "Signal peptide"  
 FT Protein /note= "Extracellular domain, preferably residues 26-544"  
 FT /note= "994  
 FT Domain /note= "Mature murine neural kinase"  
 FT Region /note= "Ig-like domain"  
 FT /note= "239..268  
 FT Region /note= "Ig-like Nuk repeat"  
 FT /note= "330..420  
 FT Region /note= "Fibronectin type III repeat"  
 FT /note= "444..534  
 FT Domain /note= "Fibronectin type III repeat"  
 FT /note= "549..574  
 FT Binding-site /note= "Hydrophobic transmembrane domain"  
 FT /note= "600..618  
 FT /note= "SH2 domain binding site"

FT Region 601..994  
 FT /note= "Carboxy terminal"  
 FT Modified-site 604..613  
 FT /note= "Phosphorylation site"  
 FT Domain 623..888  
 FT /note= "Catalytic tyrosine kinase domain"  
 FT Binding-site 623..707  
 FT /note= "ATP binding site"  
 XX US6218356-B1.  
 XX 17-APR-2001.  
 XX 13-OCT-1995; 95US-00542635.  
 XX 29-APR-1994; 94US-00235407.  
 XX 28-APR-1995; 95WO-CA000254.  
 XX (MOUN ) MOUNT SINAI HOSPITAL CORP.  
 XX Pawson A, Henkemeyer M, Letwin K;  
 XX WPI; 2001-289845/30.  
 XX N-PSDB; AAS03812.  
 XX New composition comprising neural receptor tyrosine kinase protein useful  
 XX for inhibiting or stimulating axonogenesis, neuronal development, or  
 XX regeneration and axonal migration.  
 XX Claim 1; Fig 2; 86pp; English.  
 XX The sequence represents a mouse neural kinase (Nuk) polypeptide. The  
 XX murine Nuk locus has been mapped to the distal end of chromosome four.  
 XX The polypeptide is a novel receptor tyrosine kinase protein, and is found  
 XX to be expressed at high levels within migrating axons and is associated  
 XX with nerve fibres. It functions to regulate specific cell-cell  
 XX interactions during early development of the nervous system and in  
 XX axonogenesis. Substances which bind to the Nuk protein, particularly  
 XX ligands, may be used for stimulating or inhibiting neuronal development,  
 XX regeneration and axonal migration associated with neurodegenerative  
 XX disorders and conditions involving trauma and injury to the nervous  
 XX system. These disorders include Alzheimer's disease, Parkinson's disease,  
 XX Huntington's disease, demyelinating diseases such as multiple sclerosis,  
 XX amyotrophic lateral sclerosis, deficiency diseases such as Wernicke's  
 XX disease and nutritional polyneuropathy, progressive supranuclear palsy,  
 XX Shy Drager's syndrome, multistep degeneration, olivoponto cerebellar  
 XX atrophy, peripheral nerve damage, and ischaemia resulting from stroke.  
 XX The proteins may be used to prepare antibodies having specificity for Nuk  
 XX proteins, which can be used to diagnose or treat disorders of the nervous  
 XX system. These proteins are also used for screening agonists or  
 XX antagonists of the interactions of the Nuk proteins with binding  
 XX molecules  
 XX  
 SQ Sequence 994 AA;  
 Query Match 98.9%; Score 5130; DB 4; Length 994;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 LLLPLLAANVEETLMDSTTATAELGWNVHPSPSGHEEVSVDENNNNTTIRTYQVCNVFESSQ 69  
 DB 18 LLLPLLAANVEETLMDSTTATAELGWNVHPSPSGHEEVSVDENNNNTTIRTYQVCNVFESSQ 77  
 QY 70 NNWLRTKFIIRRGAAHRIHVMKFSVRDCSSIPSPVPGSKCTFNLYYYEADFDATKTFPN 129  
 DB 78 NNWLRTKFIIRRGAAHRIHVMKFSVRDCSSIPSPVPGSKCTFNLYYYEADFDATKTFPN 137  
 QY 130 WMENPWVKVDITAADESFSQVDLGGVRVWKINTEVRSFGPVSRSGFYLAFOYGGCMSLIA 189  
 DB 138 WMENPWVKVDITAADESFSQVDLGGVRVWKINTEVRSFGPVSRSGFYLAFOYGGCMSLIA 197  
 QY 190 VRVPYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 249

Db 198 VRVPYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 257  
 QY 250 PIGRCMKAGFEAVENGTCVRCGPGSGTFFKANQDGEACTHCPINSRTTSEGATNCVCNGY 309  
 Db 258 PIGRCMKAGFEAVENGTCVRCGPGSGTFFKANQDGEACTHCPINSRTTSEGATNCVCNGY 317  
 QY 310 YRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 369  
 Db 318 YRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 377  
 QY 370 GACTRCGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFQFASVNI 429  
 Db 378 GACTRCGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFQFASVNI 437  
 QY 430 TTNQAAPSASVIMHOVSRTVDSITLSWSQDQPNGLVDYELQYKEKSELYNATAIKSP 489  
 Db 438 TTNQAAPSASVIMHOVSRTVDSITLSWSQDQPNGLVDYELQYKEKSELYNATAIKSP 497  
 QY 490 TINTVTVOGLKAGAIYVQVRAARTVAGYGRYSGRMVFTMTAEAYQTSIQEKLPIIIGSSA 549  
 Db 498 TINTVTVOGLKAGAIYVQVRAARTVAGYGRYSGRMVFTMTAEAYQTSIQEKLPIIIGSSA 557  
 QY 550 AGLVFLIAVVIIVCNRRGFERADSEYTDKLOHYTSGHMTGPKIYIDPFTYEDNEAV 609  
 Db 558 AGLVFLIAVVIIVCNRRGFERADSEYTDKLOHYTSGHMTGPKIYIDPFTYEDNEAV 617  
 QY 610 REFAKEIDISCVKIEQVIGAGBEGEVCSGHLKLPGRKEIFVATKTLKSGVTEKQRDFLS 669  
 Db 618 REFAKEIDISCVKIEQVIGAGBEGEVCSGHLKLPGRKEIFVATKTLKSGVTEKQRDFLS 677  
 QY 670 EASIMGQFDHPNVIHLEGVVTKSTPVMIIITEFMENGLSDSLFRQNDGQFTVIOLVGMRLG 729  
 Db 678 EASIMGQFDHPNVIHLEGVVTKSTPVMIIITEFMENGLSDSLFRQNDGQFTVIOLVGMRLG 737  
 QY 730 IAAGMYLADNMVYVHRDLAARNILVNSNLVCKVDFGLSRFLBDDTSDPTTYSALGKIP 789  
 Db 738 IAAGMYLADNMVYVHRDLAARNILVNSNLVCKVDFGLSRFLBDDTSDPTTYSALGKIP 797  
 QY 790 IRTAPEAIQYRKFTSASDVWSYGI VNWVMSYGERPYMDMTNQDVINAEQDYRLPPPM 849  
 Db 798 IRTAPEAIQYRKFTSASDVWSYGI VNWVMSYGERPYMDMTNQDVINAEQDYRLPPPM 857  
 QY 850 DCPSSALHQLMDCQKDRNHRPKFGQIVNTLDKMIENPNLSLKAWAPLSSGINLPLDRTI 909  
 Db 858 DCPSSALHQLMDCQKDRNHRPKFGQIVNTLDKMIENPNLSLKAWAPLSSGINLPLDRTI 917  
 QY 910 PDYTSFNTVDWELEAIKMGQYKESFANAGTSPDVVVSQMMEDILRLGVTLAGHOKKILN 969  
 Db 918 PDYTSFNTVDWELEAIKMGQYKESFANAGTSPDVVVSQMMEDILRLGVTLAGHOKKILN 977  
 QY 970 SIQVMRAQMNQIOSVEV 986  
 Db 978 SIQVMRAQMNQIOSVEV 994  
 RESULT 8  
 AAR87018  
 ID AAR87018 standard; protein; 994 AA.  
 XX AAR87018;  
 XX 19-MAR-1996 (first entry)  
 DT Receptor tyrosine kinase (neural kinase).  
 XX Receptor tyrosine kinase; neural kinase; Nuk; axon; axonogenesis;  
 XX nerve disorder.  
 OS Mus musculus.  
 XX Key Location/Qualifiers  
 FT Peptide i..26  
 FT /label= Sig\_peptide

```

FT Region 27. 548
FT /label= Extracellular_region
FT /note= "the extracellular region (amino acids 27-548)
FT includes an N-terminal Ig-like domain and an Ig-like Nuk
FT repeat"
FT Region 330. 420
FT /label= FNIII
FT /note= "fibronectin type III repeat"
FT 444. 534
FT /label= FNIII
FT /note= "fibronectin type III repeat"
FT 549. 574
FT /label= Transmembrane_region
FT 575. 994
FT /label= Cytoplasmic_region
FT 623. 707
FT /label= Tyrosine-kinase_catalytic_domain
XX WO9530326-A1.
XX 09-NOV-1995.
XX 28-APR-1995; 95WO-CA000254.
XX 29-APR-1994; 94US-00235407.
XX (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX Pawson A, Henkemeyer M, Letwin K;
XX WPI; 1995-393299/50.
XX N-PSDB; AAT07308.
XX
XX DNA encoding neural receptor tyrosine kinase - useful in gene therapy of
XX nerve disorders, and for diagnosis and identification of therapeutic
XX agents.
XX Claim 1; Page 70-74; 103pp; English.
XX
XX A novel receptor tyrosine kinase (AAR87018), designated neural kinase
XX (Nuk) (AAR87018), is encoded by cDNA (AAT07308) obt'd from a mouse embryo
XX library. Nuk is expressed in migrating axons and is involved in cell-cell
XX interactions and axonogenesis in development of the nervous system. Nuk
XX or its fragments (pref. amino acids 26-548 or 601-994) are used to
XX identify (ant)agonists of the (activated) receptor tyrosine kinase as a
XX means of treating nerve disorders and damage, or to raise antibodies used
XX to monitor axon migration and nerve cell interactions
XX
XX Sequence 994 AA;
XX
XX Query Match 98.8%; Score 5126; DB 2; Length 994;
XX Best Local Similarity 99.4%; Pred. No. 0;
XX Matches 971; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
XX 10 LLLLPLLAABEETLMDSTTATAELGMMVHPSPGWEESVGYDENNMNTIRTYQVCNPFESSQ 69
XX |||||
XX 18 LLLLPLLAABEETLMDSTTATAELGMMVHPSPGWEESVGYDENNMNTIRTYQVCNPFESSQ 77
XX |||||
XX 70 NNMLRTKFIERRGAHRTHVEMKFSVRDCSSIPSPVPGSKETENLYYYEADFDGATKTFPN 129
XX |||||
XX 78 NNMLRTKFIERRGAHRTHVEMKFSVRDCSSIPSPVPGSKETENLYYYEADFDGATKTFPN 137
XX |||||
XX 130 WMENPWVKVDITIAADESFSQVDLGGRVWKINTEVRSFGPVSRSGFYLAFOYGGCMSLIA 189
XX |||||
XX 138 WMENPWVKVDITIAADESFSQVDLGGRVWKINTEVRSFGPVSRNGFYLAFOYGGCMSLIA 197
XX |||||
XX 190 VRVPYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 249
XX |||||
XX 198 VRVPYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 257
XX |||||
XX 250 PIGRCMKAGFEAVENGTVCRCPSGTFKANOQDEACTHCPINSRTTSEGATNCVCNGY 309
XX |||||
XX 258 PIGRCMKAGFEAVENGTVCRCPSGTFKANOQDEACTHCPINSRTTSEGATNCVCNRY 317
XX |||||

```

```

310 YRADLDPLDMPTTIPSAPOAVISSVNETSIMLEWTTPRDSGGREDLVYNIICKSCGSGR 369
318 YRADLDPLDMPTTIPSAPOAVISSVNETSIMLEWTTPRDSGGREDLVYNIICKSCGSGR 377
370 GACTRCGDNVQYAPRQLGLTEPRIYISDLLAHTQYTFEIOAVNGVTOQSPPOFASVNI 429
378 GACTRCGDNVQYAPRQLGLTEPRIYISDLLAHTQYTFEIOAVNGVTOQSPPOFASVNI 437
430 TTNOAPSASVIMHOVSRTVDSITLWSQDPQNGVILDYELQYKEKELSEYNATAIKSP 489
438 TTNOAPSASVIMHOVSRTVDSITLWSQDPQNGVILDYELQYKEKELSEYNATAIKSP 497
490 TTTVTVOGLKAGAIYVQVRARTVAGYGRYSGRMVFTQMTAEAYQTSIQEKLPLIIGSSA 549
498 TTTVTVOGLKAGAIYVQVRARTVAGYGRYSGRMVFTQMTAEAYQTSIQEKLPLIIGSSA 557
550 AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNEAV 609
558 AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNEAV 617
610 REFAKEIDISCVKIEOVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLS 669
618 REFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLS 677
670 EASIMGQFDHPNVIHLEGVVTKSTPVMIITEFMENGSLDSFLRQNDGQFTVIQLVGMRLG 729
678 EASIMGQFDHPNVIHLEGVVTKSTPVMIITEFMENGSLDSFLRQNDGQFTVIQLVGMRLG 737
730 IAAGMKYLADNMVYVHRDLAARNILVNSNLVKYSDFGSLRFLDSDTSDPYTTSALGSKIP 789
738 IAAGMKYLADNMVYVHRDLAARNILVNSNLVKYSDFGSLRFLDSDTSDPYTTSALGSKIP 797
790 IRTAPEAIQYRKFTSASDVMSYGIVMWEVMSYGERPYWDMTQDVNATEQDYRLPPPM 849
798 IRTAPEAIQYRKFTSASDVMSYGIVMWEVMSYGERPYWDMTQDVNATEQDYRLPPPM 857
850 DCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLLDRTI 909
858 DCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLLDRTI 917
910 PDYTSNTVDWEUAEIATMGQYKESFANAGTSPDVSVSQMMEDILRLGVTLAGHQKILN 969
918 PDYTSNTVDWEUAEIATMGQYKESFANAGTSPDVSVSQMMEDILRLGVTLAGHQKILN 977
970 SIQVMEAAQMNQIOSVEV 986
978 SIQVMEAAQMNQIOSVEV 994

```

```

RESULT 9
AAR85089
ID AAR85089 standard; protein; 970 AA.
XX AAR85089;
XX AC
XX XX
XX DT 16-APR-1996 (first entry)
XX XX
XX DE EPH-like receptor protein tyrosine kinase HEKS.
XX XX
XX KW EPH-like receptor protein tyrosine kinase; PTK; HEKS;
XX human eph-like kinase; therapy; diagnosis; vector; antibody.
XX OS Homo sapiens.
XX XX
XX PN WO9528484-A1.
XX XX
XX PD 26-OCT-1995.
XX XX
XX PF 14-APR-1995; 95WO-US004681.
XX XX
XX PR 15-APR-1994; 94US-00229509.
XX XX

```

(AMGE-) AMGEN INC.  
 Fox GM, Welcher AA, Jing S;  
 WPI; 1995-373799/48.  
 N-PSDB; AAT02946.  
 New nucleic acid encoding Eph-like receptor tyrosine kinase(s) - and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation or prodn.  
 Claim 18; Page 46-49; 133pp; English.  
 4 Novel human Eph-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (AAR85089-92), respectively, were identified following isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken Eph-like receptors Cdk5, Cdk7 and Cdk8. HEK11 shows no homology to any known Eph-like receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced by expression of encoding sequences in prokaryotic or eucaryotic host cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HEK receptors, or therapeutically to modulate the activation of cell-associated receptors. Soluble HEK5 receptor may affect primarily brain and pancreatic cells  
 Sequence 970 AA:  
 Query Match 98.2%; Score 5093; DB 2; Length 970;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;  
 15 LLA VEETLMDSTTATAE LGMVHPSPGMEVSGYDENMTIRTYQVCNVFESSQNNWLR 74  
 1 LLA VEETLMDSTTATAE LGMVHPSPGMEVSGYDENMTIRTYQVCNVFESSQNNWLR 60  
 75 TKFIRRRGAIRIHVEMKFSVRDCCSSIPSPGCKETENLYYEADFD SATKTFPNWMEP 134  
 61 TKFIRRRGAIRIHVEMKFSVRDCCSSIPSPGCKETENLYYEADFD SATKTFPNWMEP 120  
 135 WVKVDTTAADESFQVDLGRVVKINTEVSRFVSRSGFYLAPODYGGCMSLIARVVFY 194  
 121 WVKVDTTAADESFQVDLGRVVKINTEVSRFVSRSGFYLAPODYGGCMSLIARVVFY 180  
 195 RKCPRITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRC 254  
 181 RKCPRITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRC 240  
 255 MCKAGFAVENGTVCRCGPGSTFKANQDGAETHCPINRTTSEGATNCVCRNGYRADL 314  
 241 MCKAGFAVENGTVCRCGPGSTFKANQDGAETHCPINRTTSEGATNCVCRNGYRADL 300  
 315 DPLDMPCTTIPSAQVAISSVNETSLMWTTPRDSGREDLVNIIICKSGSGRGACTR 374  
 301 DPLDMPCTTIPSAQVAISSVNETSLMWTTPRDSGREDLVNIIICKSGSGRGACTR 360  
 375 CGDNVQVAPROGLGTEPRYIISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNITNQA 434  
 361 CGDNVQVAPROGLGTEPRYIISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNITNQA 420  
 435 APSAVSMHVSRTVDSITLWSQDPNGVILDYELQYVEKELSEYNATAIKSPNTVT 494  
 421 APSAVSMHVSRTVDSITLWSQDPNGVILDYELQYVEKELSEYNATAIKSPNTVT 480  
 495 VQGLKAGAIYVQVARTVAGYSGKMWPTMTAEYQTSIQEKLPLIIGSSAAGLVF 554  
 481 --GLKAGAIYVQVARTVAGYSGKMWPTMTAEYQTSIQEKLPLIIGSSAAGLVF 538  
 555 LIAVVTIAVNCRRGFRADSEYTDKLOHTYSGHMTFCMKIYIDPFTYEDPNEAVREPAK 614  
 539 LIAVVTIAVNCRRGFRADSEYTDKLOHTYSGHMTFCMKIYIDPFTYEDPNEAVREPAK 598

QY 615 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDFLSEASIM 674  
 DB 599 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDFLSEASIM 658  
 QY 675 GQFDHENVHLEGVVTKSTPVMIIITEFMENGLSDSFLRNDGQFTVIQVLVGMRLGIAAGM 734  
 DB 659 GQFDHENVHLEGVVTKSTPVMIIITEFMENGLSDSFLRNDGQFTVIQVLVGMRLGIAAGM 718  
 QY 735 KYLADMNYYVHRDLAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTVTSALGKIPIRWTA 794  
 DB 719 KYLADMNYYVHRDLAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTVTSALGKIPIRWTA 778  
 QY 795 PEAIQYRKFTSADSVMSYGI VMMVEVMSYGERPYWMTNQDVINAIBQDYLRLPPPMDCPSA 854  
 DB 779 PEAIQYRKFTSADSVMSYGI VMMVEVMSYGERPYWMTNQDVINAIBQDYLRLPPPMDCPSA 838  
 QY 855 LHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPDRTIPDYS 914  
 DB 839 LHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPDRTIPDYS 898  
 QY 915 FNTVDEWLEAIKMGQYKESFANAGTSDVVSQMMEDILRLGVTLAGHKKILNSIQVM 974  
 DB 899 FNTVDEWLEAIKMGQYKESFANAGTSDVVSQMMEDILRLGVTLAGHKKILNSIQVM 958  
 QY 975 RAQMNOIQSVEV 986  
 DB 959 RAQMNOIQSVEV 970  
 RESULT 10  
 AAR75712  
 ID AAR75712 standard; protein; 995 AA.  
 AC AAR75712;  
 XX 25-MAR-2003 (revised)  
 DT 11-NOV-1995 (first entry)  
 DE XX  
 DE XX  
 KW Eph-related PTK Cdk5.  
 XX Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis; prognosis.  
 XX Gallus sp.  
 OS WO9515375-A1.  
 PN 08-JUN-1995.  
 PD 07-SEP-1994; 94WO-US010140.  
 XX 03-DEC-1993; 93US-00162809.  
 PR (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX Pasquale EB, Sajjadi FG;  
 PI WPI; 1995-215256/28.  
 XX N-PSDB; AAO90660.  
 DR Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
 XX cancer.  
 PT Disclosure; Page 92-96; 129pp; English.  
 PS Probes derived from the Eph-related PTKs Cdk4 (AAQ90659) and Cdk5  
 XX (AAQ90660) were used to isolate novel cDNA clones (AAQ90652-58, AAQ90661-  
 CC 62) from chicken embryo and embryonic brain libraries. (Updated on 25-MAR  
 CC -2003 to correct PN field.)  
 SQ Sequence 995 AA;  
 Query Match 96.3%; Score 4993.5; DB 2; Length 995;  
 Best Local Similarity 95.8%; Pred. No. 0;

Matches	937; Conservative	28; Mismatches	12; Indels	1; Gaps	1;
Qy	10	LLLLPLAAVEETLMDSTTATAELGMMVHPSPGSEVSGYDENMNTIRTYQVCNVFESSQ	69		
Db	18	LALLPLAAVEETLMDSTTATAELGMMVHPSPGSEVSGYDENMNTIRTYQVCNVFESSQ	77		
Qy	70	NNWLRTKPIRRGAHRIHVEMKFSVRDCSSIPSPVGSCKETFNLYYYEADPDSATKTFPN	129		
Db	78	NNWLRTKYIRRGGAHRIHVEMKFSVRDCSSIPNPVGSCKETFNLYYYESDPSATKTFPN	137		
Qy	130	WMENPMVKVDTTAADESPQVLDGGRVVKINTEVSPGVSRSGFYLAFOQYGGCMSLIA	189		
Db	138	WMENPMVKVDTTAADESPQVLDGGRVVKINTEVSPGVSKNGFYLAFOQYGGCMSLIA	197		
Qy	190	VRVFKKCPRIITONGAIFOETLSGAESTSLVAARGSCIANAEEDVDPVKLYCNGDGEWL	249		
Db	198	VRVFKKCPRIITONGAIFOETLSGAESTSLVAARGTCISNAEEVDVPIKLYCNGDGEWL	257		
Qy	250	PIGRCKMCKAFRAVNGTVCRGCPGTFKANGDGAETHCPINSTRTTSEGTATNCVCRNGY	309		
Db	258	PIGRCKMCRPGYSEVNGTVCRGCPGTFKASQDGGCVHCPINSTRTTSEGTATNCVCRNGY	317		
Qy	310	YRADLDPLDMPCTTIPSAQVAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSCGSGR	369		
Db	318	YRADADPVDMPCTTIPSAQVAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSCGSGR	377		
Qy	370	GACTRCGDNVQAPROLGLTEPRIVISDIIAHTQYTFEIQAVNGVTDQSPSPQASVNI	429		
Db	378	GACTRCGDNVQAPROLGLTEPRIVISDIIAHTQYTFEIQAVNGVTDQSPSPQASVNI	437		
Qy	430	TTNQAAPSIVSMHQSRTVDSITLSWSPQDPNGVILDYELQYKEKLSBYNATAIKSP	489		
Db	438	TTNQAAPSIVSMHQSRTVDSITLSWSPQDPNGVILDYELQYKEKLSBYNATAIKSP	497		
Qy	490	TNTVTVOGLKAGNIYVQVRAATVAGYSGKMTFQMTAEAYQTSQEKPLIIGSSA	549		
Db	498	TNTVTVOGLKAGNIYVQVRAATVAGYSGKMTFQMTAEAYQTSQEKPLIIGSSA	557		
Qy	550	AGLVFLIAVVTIAVCN-RRGPERADSEYTDKLQHTSGHMTPGMKIYIDPFTVEDPNEA	608		
Db	558	AGLVFLIAVVTIAVCN-RRGPERADSEYTDKLQHTSGHMTPGMKIYIDPFTVEDPNEA	617		
Qy	609	VREFAKEIDISCVKIQQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQRDFL	668		
Db	618	VREFAKEIDISCVKIQQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQRDFL	677		
Qy	669	SEASIMQGDHPNVHLEGVVTKSPWMIITFEMNGSLDSFLRQNDQOFTVIQVGLMR	728		
Db	678	SEASIMQGDHPNVHLEGVVTKSPWMIITFEMNGSLDSFLRQNDQOFTVIQVGLMR	737		
Qy	729	GIAAGKYLADNMVYHVRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPYTSALGGKI	788		
Db	738	GIAAGKYLADNMVYHVRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPYTSALGGKI	797		
Qy	789	PIRWTAPAIQYKFTSASDVMSYGIYVMEVMSYGERPYWDMTNDVINAIEQDYRLPPP	848		
Db	798	PIRWTAPAIQYKFTSASDVMSYGIYVMEVMSYGERPYWDMTNDVINAIEQDYRLPPP	857		
Qy	849	MDCPSALHQLMDCWQKQNRHPRKFGQIVNTLDKMRPNLSLKAVAPLSSGGINPLDRT	908		
Db	858	MDCPSALHQLMDCWQKQNRHPRKFGQIVNTLDKMRPNLSLKAVAPLSSGGINPLDRT	917		
Qy	909	IPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRGVTLAGHOKKIL	968		
Db	918	IPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRGVTLAGHOKKIL	977		
Qy	969	NSIQVMRAQMNQIQSVEV 986			
Db	978	NSIQVMRAQMNQIQSVEV 995			

RESULT 11  
AAR75709

430 TTNQAPSASIMHQVSRITSLWSQDPQNGVILDYELQYKEKELSEYNATAIKSP 489  
438 TTNQAPSASIMHQVSRITSLWSQDPQNGVILDYELQYKEKELSEYNATAIKSP 497  
490 TTTVQGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSSA 549  
498 TTTVQGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSSA 557  
550 AGLVFLAVVIAVCN- RGFPERADSEYTDKLOHTSGH-----MTPG 592  
558 AGLVFLAVVIAVCN- RGFPERADSEYTDKLOHTSGH-----MTPG 617  
593 MKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAI 652  
618 MKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAI 677  
653 KTLKSGYTEKQRDFLSEASIMQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLR 712  
678 KTLKSGYTEKQRDFLSEASIMQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLR 737  
713 QNDGQFTVIQVGLMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVKYSDFLSFLR 772  
738 QNDGQFTVIQVGLMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVKYSDFLSFLR 797  
773 DDTSDPTYSALGGKIPIRWTAPPAIQRKFTSASDVMSYGVIMVWMSYGERPYWDMTN 832  
798 DDTSDPTYSALGGKIPIRWTAPPAIQRKFTSASDVMSYGVIMVWMSYGERPYWDMTN 857  
833 QDVINAIEQYRLPPPPMDPCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMKIRNPNLSKA 892  
858 QDVINAIEQYRLPPPPMDPCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMKIRNPNLSKA 917  
893 MAPLSSGINLPLDRTIPDYTSFNTVDWLEAIKWGOYKESFANAGFTSFDVVSQMMED 952  
918 MAPLSSGINLPLDRTIPDYTSFNTVDWLEAIKWGOYKESFANAGFTSFDVVSQMMED 977  
953 ILRLGVTLAGHQKILNSIQVMRAQNMQIQSVEV 986  
978 ILRLGVTLAGHQKILNSIQVMRAQNMQIQSVEV 1011

RESULT 12  
ADO28627  
ID ADO28627 standard; protein; 969 AA.  
XX AC ADO28627;  
XX DT 12-AUG-2004 (first entry)  
XX DE Human EPHB2 protein SEQ ID NO:56.  
XX OS Homo sapiens.  
XX KW high-grade dysplasia; HGD; oesophageal adenocarcinoma;  
XX KW neo-plastic transformation; cancer; cytostatic; gene therapy; human;  
XX KW EPHB2; chromosome 1.  
XX OS Homo sapiens.  
XX PN W0200404178-A2.  
XX PD 27-MAY-2004.  
XX PF 13-NOV-2003; 2003WO-US036260.  
XX PR 13-NOV-2002; 2002US-0425813P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Smith V;  
XX DR WPI; 2004-420319/39.  
XX DR N-PSDB; ADO28626.  
XX

PT Detecting of high-grade dysplasia in cells of a mammalian tissue sample  
PT comprises establishing the level of expression in the test tissue sample  
PT of the genes.

PS Example 4; SEQ ID NO 56; 256pp; English.

XX The present invention describes a method for detecting high-grade  
CC dysplasia (HGD) in cells of a mammalian tissue sample. Also described:  
CC (1) identifying an oesophageal tissue susceptible to oesophageal  
CC adenocarcinoma; (2) determining the predisposition of a mammalian tissue  
CC to a neo-plastic transformation by detecting HGD in cells of the tissue;  
CC and (3) detecting cancer in a patient. The method can be used in  
CC detecting HGD and cancer in cells of a mammalian tissue sample. The  
CC methods and compositions of the present invention can be used in treating  
CC and preventing HGD and cancer, and in gene therapy. The present sequence  
CC represents human EPHB2, which is used in the exemplification of the  
CC present invention. The human EPHB2 gene is located on chromosome 1.

XX Sequence 969 AA;

Query Match 95.1%; Score 4936; DB 8; Length 969;

Best Local Similarity 98.3%; Pred. No. 0;

Matches 969; Conservative 1; Mismatches 0; Indels 16; Gaps 16;

QY 2 ALRRLGAAALLLPLLAABVETLMDSTTATAELGVMVHPSPGMEVSGYDENMTTIRYQV 61  
DB 1 ALRRLGAAALLLPLLAABVETLMDSTTATAELGVMVHPSPGMEVSGYDENMTTIRYQV 59  
QY 62 CNVFESSQNNWLTKEIRRGARHIVEMKFSVRDCSSIPSVPGSCKEFNLVYYEADFD 121  
DB 60 CNVFESSQNNWLTKEIRRGARHIVEMKFSVRDCSSIPSVPGSCKEFNLVYYEADFD 118  
QY 122 SATKTPNNWENPVKVDITIADESQVLDLGRVMKINTEVRSFGVSRSGFYLAQDY 181  
DB 119 SATKTPNNWENPVKVDITIADESQVLDLGRVMKIN- EVRSFGVSRSGFYLAQDY 177  
QY 182 GGCMSLIAVRVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYC 241  
DB 178 GGCMSLIAVRVFRKCPRIIQNGAIFQETLSGAESTS-VAARGSCIANAEVDVPKLYC 236  
QY 242 NGDGWLVPIGRCMCKAGFEAVENGIVCRGCPSGT-KANQGDRACTHCPINSTRTSEGAT 301  
DB 237 NGDGWLVPIGRCMCKAGFEAVENGIVCRGCPSGT- KANQGDRACTHCPINSTRTSEGAT 295  
QY 302 NCVCRNGYVRADLDPLDMPCTTIPSAQVAVISSVNETSLMLEWTPPRDSGREDLVNII 361  
DB 296 NCVCRNGYVRADLDPLDMPCTTIPSAQVAVISS- NETSLMLEWTPPRDSGREDLVNII 354  
QY 362 CKSCGSGRGACTRCGDNVQVAPRQLGLTEPRYIISDLAHTQYTFEIQAVNGVTDQSPFS 421  
DB 355 CKSCGSGRGACTRCGDNVQVAPRQLGLTEPR- YISDLAHTQYTFEIQAVNGVTDQSPFS 413  
QY 422 PQFASVNIITNQAPSASIMHQVSRITSLWSQDPQNGVILDYELQYKEKELSEY 481  
DB 414 PQFASVNIITNQAPSASIMHQVSRITSLWSQDPQNGVILDYELQYKEKELSEY 472  
QY 482 NATAIKSPNTVTVQGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKL 541  
DB 473 NATAIKSPNTVTVQGLKAGAIYVQV-ARTVAGYGRYSGKMYFQMTAEAYQTSIQEKL 531  
QY 542 PLIIGSSAAGLVFLIAVWIAIVCNRRGFERADSEYTDKLOHTSGHMTGMIYIDPFT 601  
DB 532 PLIIGSSAAGLVFLIAVWIAIVCNRRGFERADSEYTDKLOHTSGHMTGMIYIDPFT 591  
QY 602 YEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKLSGYTE 661  
DB 592 YEDPNEAVREFAKEIDISCVKI- QVIGAGEFGEVCSGHLKLPGRKREIFVAIKLSGYTE 650  
QY 662 KORRDFLSEASIMQFDPNVIHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVI 721  
DB 651 KORRDFLSEASIMQFDPN- IHLEGVVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVI 709  
QY 722 QLVGMRLGRTAGMKYLADMYVHRDLAARNILVNSNLVKYSDFLSFLRLEDDTSDPTYT 781



|||||  
710 QLVGMLRGIAGMKYLAD-NYVHRDLAARNILVNSLVCKVSDFLSFLFDDTSDPTYT 768  
782 SALGGKIPIRWTAPEAIQYRKFTSASDWSYGIWVNEVMSYGERPYWDMNQDVINAIEQ 841  
769 SALGGKIPIRWTAPEA-QYRKFTSASDWSYGIWVNEVMSYGERPYWDMNQDVINAIEQ 827  
842 DYRLPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDMKIRNPNLSLKAMAPLSSGIN 901  
828 DYRLPPMDCPSAL-QLMMLDCWQKDRNHRPKFGQIVNTLDMKIRNPNLSLKAMAPLSSGIN 886  
902 LPLDRTIPDYSFNTVDWLEATKMGQYKESFANAGFTSFDVVSQMMEDILRLGYTLA 961  
887 LPLDRTIPDYT-FNTVDWLEATKMGQYKESFANAGFTSFDVVSQMMEDILRLGYTLA 945  
962 GHQKKILNSIQVRAQNNQIOSVEV 986  
946 GHQKKILNSI-VRAQNNQIOSVEV 969  
RESULT 13  
ADE63400  
ID ADE63400 standard; protein; 984 AA.  
XX  
AC ADE63400;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
XX Rat Protein CAA31777, SEQ ID NO 9339.  
XX  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
XX Rattus norvegicus.  
XX  
XX WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-033347P.  
XX  
XX (GHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX  
XX WPI; 2003-268312/26.  
XX GENBANK; CAA31777.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 984 AA;  
Query Match 75.8%; Score 3934.5; DB 7; Length 984;  
Best Local Similarity 73.9%; Pred. No. 1.4e-287;  
Matches 720; Conservative 128; Mismatches 125; Indels 1; Gaps 1;  
QY 11 LLLPLLAABEETLMDSTTATAEALGMVHPHSGVEVSGYDENMNTIRTYQVNVFESSON 70  
DB 10 LLASAVAAMEETLMDRTATAEALGWTANPASGWEVSGYDENLNTIRTYQVNVFEPNQ 69  
QY 71 NWLRTKFIERRGAHRIHVEMKFSVRDCSSIPSPGSCKETFNLYYYEADFSATKTPNW 130  
DB 70 NWLLTTFINRRGAHRIYTEMFTVRDCSSLPNPGSCKETFNLYYYETDSVIATKSAFW 129  
QY 131 MENPWWKVDITAADESFQVDLGLGRVWKINTEVRSFGPVSRSFGYLAFOYGGCMSLIIV 190  
DB 130 SEAPYKLVDTIAADESFQVDLGLGRVWKINTEVRSFGPVSFGPLTRNGFYLAFOYGGCMSLIIV 189  
QY 191 RVFRRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVP 250  
DB 190 RVFFKKCPISIVQNFVFPETMTCAESTSLVIARGTCPNAAEVDVPIKLYCNGDGEMLVP 249  
QY 251 IGRCKAGFEAVENGTVCGPCSGTFKANOGBEACTHCPIINGRTTSEGATNCVCRNGYY 310  
DB 250 IGRCTCKAGYEP-ENSVACKACAPAGTFKASQEAEGCSHCPSNRSRSPSEASPTCTRTGY 308  
QY 311 RADLDPLDMPCCTTIPSAPOAVISSVNETSLMLWTTPRDSGGREDLVYNIICKSCSGRG 370  
DB 309 RADFDPEVACTSVPGSPRNVISIVNETSILLHHPRETGGRDDVYNIICKCRADRR 368  
QY 371 ACTRCGDNVQYARQLGLTEPRIYISDLAHTOYTFEIQAVNGVTQSPSPFASVNIIT 430  
DB 369 SCSCDDNVEFVPRQLGLTECRVSISSLWAHTPTFTDIQAINGVSSKSPFPQHVSNIT 428  
QY 431 TNOAAPSASVIMHQVSRVDSITLSWSQPPQNGVILDYELQYKELSEYNATAIKSPT 490  
DB 429 TNOAAPSSTVPIMHQVSATMRISITLSWPQEPQNGIILDYBIRYKEHNFNSMARSQT 488  
QY 491 NTVTVOGLKAGAIYVQVRARTVAGYGRYSKAYFOTMTEAEYQTSIQEKLPLIGSSAA 550  
DB 489 NTARIDGLRPMGVYVQVRARTVAGYGRYSKAYFOTMTEAEYQTSIQEKLPLIGSSAA 548  
QY 551 GLVFLIAVVVIAIVCNRRGFERADSEYTKLQHYTSGHMTFPGMKIYIDPTTYEDPNEAVR 610  
DB 549 GVVFVSVLVAISVCSKRAYSKAYVSDKLQHYSTGRSGPMKIYIDPTTYEDPNEAVR 608  
QY 611 EFAKEIDISCKIEQVIGAGEFGEVCSGHKLPGKREIFVAIKLKSQGYTEKORRDLSE 670  
DB 609 EFAKEIDVSPKIEEIVIGAGEFGEVCSGHKLPGKREIYVAIKLKSQGYTEKORRDLSE 668  
QY 671 ASITMGQFDHNVTHLGSVVTKSTPVMILITFPMNGSLDSFLRNDQDGTFTVQLVGLMURGI 730  
DB 669 ASITMGQFDHNVTHLGSVVTKSTPVMILITFPMNGSLDSFLRNDQDGTFTVQLVGLMURGI 728  
QY 731 AAGMKYLADNVYVHRDLAARNILVNSLVCKVSDFLSFLFDDTSDPTYSALGGKIP 790  
DB 729 AAGMKYLSENVYVHRDLAARNILVNSLVCKVSDFLSFLFDDTSDPTYSALGGKIP 788  
QY 791 RWTAPAIQYRKFTSADWSYGIWVNEVMSYGERPYWDMNQDVINAIEQVRLPPMD 850

Db 789 RWTAPAIYKFKTSASDVMSYGIWMEVMSFGRPYWDMNSQDVINAIBQDYRLPPMD 848  
Qy 851 CPSALHQLMLDCWKDRNRHFKQIVNTLDKMRNPNLSKAMAPLSSGINLPLDRTIP 910  
Db 849 CPAALHQLMLDCWKDRNSRFRFAEIVNTLDKMRNPNLSKATVATITAVPSQPLDPSIP 908  
Qy 911 DYTSTNTVDWELEAKMGQYKESFANAGFTSFVVSQMMEDILRLGVLGAGHKKILNS 970  
Db 909 DFTAFTVDDWLSAIAKMWQYRDSFLTAGFTSLQVLTQWTSBELLRIGVTLGAGHKKILSS 968  
Qy 971 IQWMRAQWNOQSV 984  
Db 969 IHSMRVQWNOQSPV 982

## RESULT 14

AD883380  
ID AD883380 standard; protein; 984 AA.

AC AD883380;

XX 29-JAN-2004 (first entry)

XX Rat Protein P09759, SEQ ID NO 10974.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEMO ) GEN HOSPITAL CORP.

XX (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P09759.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity in an animal of one or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
XX modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 984 AA;

Query Match 75.8%; Score 3934.5; DB 7; Length 984;  
Best Local Similarity 73.3%; Pred. No. 1.4e-287;  
Matches 720; Conservative 128; Mismatches 125; Indels 1; Gaps 1;

Qy 11 LLLPLLAABEETLMDSTTATAELGMVHPHPSGWEVSGYDENNMNTTIRTVQCNVFPSSQN 70  
Db 10 LLASAVAMEETLMDTETATAELGTANTPASGWEVSGYDENLNTIRTVQCNVFPNQN 69  
Qy 71 NWLRTKFIIRRGAAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYEADPSATKTFPPNW 130  
Db 70 NWLLTTFINRRGAHRIYTEMFTVRDCSSLPNVPGCKETFNLYYEADPSATKTFPPNW 129  
Qy 131 MENPWKVDITIAADESFQVDLGGRYMKINTVRSFSPVSRSGFYLAFODYGGCMSLIAY 190  
Db 130 SEAPYLKVDITIAADESFQVDLGGRYMKINTVRSFSPVSRSGFYLAFODYGGCMSLIAY 189  
Qy 191 RVFRRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDDVPKILYCNCGDGEWLP 250  
Db 190 RVFRRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDDVPKILYCNCGDGEWLP 249  
Qy 251 IGRCKAGYEP-ENSVACKACPAKAGTFCASQAEAGSHCPSPSRSPSEASPICTCTGY 310  
Db 250 IGRCKAGYEP-ENSVACKACPAKAGTFCASQAEAGSHCPSPSRSPSEASPICTCTGY 308  
Qy 311 RADLPLDMPCTTIPSAQAQAVISSVNETSLMLTWTTPRDSGGREDLVYNIICKSCSGRG 370  
Db 309 RADLPLDMPCTTIPSAQAQAVISSVNETSLMLTWTTPRDSGGREDLVYNIICKSCSGRG 368  
Qy 371 ACTRCGDNVQAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNI 430  
Db 369 SCSCDDNVFVPRQLGLTECRVSISSLAHTPTFTDIAINGVSSKSPPPQHVSNIT 428  
Qy 431 TNOAARSAVIMHOVSRTVDSITLWSQDOPNGVILDYELQYKELSEYNATATKSPT 490  
Db 429 TNOAARSAVIMHOVSRTVDSITLWSQDOPNGVILDYELQYKELSEYNATATKSPT 488  
Qy 491 NTVTVOGLKAGAIYVQVRAARTVAGYSGKMYFOTMTAEAYQTSIQEKLPIIIGSSAA 550  
Db 489 NTARIQGLRPGWVYVQVRAARTVAGYSGKMYFOTMTAEAYQTSIQEKLPIIIGSSAA 548  
Qy 551 GLVFLIAVVIATVCMNRGFERADSEYTDKLQHYTSGHMTGPMKIYIDPTYEDPNEAVR 610  
Db 549 GVVVSVLSVAISVCSKRAYSKAYSVYDGLQHYTSGHMTGPMKIYIDPTYEDPNEAVR 608  
Qy 611 EFAKEIDISCKIEQVIGAGEFGEVCSGHLKPKKEIFVAIKTKSGYTEKORRFLSE 670  
Db 609 EFAKEIDISCKIEQVIGAGEFGEVCSGHLKPKKEIFVAIKTKSGYTEKORRFLSE 668  
Qy 671 ASIMGQFDPHNVHLEGVVTKSPVMIITEFMENGLDSFLRQNDQGFVQVQLVGLMRLGI 730  
Db 669 ASIMGQFDPHNVHLEGVVTKSPVMIITEFMENGLDSFLRQNDQGFVQVQLVGLMRLGI 728  
Qy 731 AAGMKYLADNMVYVHRLAARNILVNSLVCKVSDFGLSRFLSDTSDPTYSALGKIP 790  
Db 729 AAGMKYLADNMVYVHRLAARNILVNSLVCKVSDFGLSRFLSDTSDPTYSALGKIP 788  
Qy 791 RWTAPAIYKFKTSASDVMSYGIWMEVMSFGRPYWDMNSQDVINAIBQDYRLPPMD 850  
Db 789 RWTAPAIYKFKTSASDVMSYGIWMEVMSFGRPYWDMNSQDVINAIBQDYRLPPMD 848  
Qy 851 CPSALHQLMLDCWKDRNRHFKQIVNTLDKMRNPNLSKAMAPLSSGINLPLDRTIP 910  
Db 849 CPAALHQLMLDCWKDRNSRFRFAEIVNTLDKMRNPNLSKATVATITAVPSQPLDPSIP 908

Qy 911 DYTSFNTVDEWLEAKNQYKESFANAGTSTFDVVSQMMEDILRLGVTLGAGHOKKILNS 970  
Db 909 DFTAFITVDDWLSAIAKMWQYRDSFLTGTSTSLQVLTQWTSDDLRLGVTLGAGHOKKILNS 968  
Qy 971 IQVRAQWQIQSV 984  
Db 969 IHSNRVQWQNSPSV 982

## RESULT 15

AAR44513  
ID AAR44513 standard; protein; 984 AA.

XX AC  
XX AC

XX DT 16-JUN-1994 (first entry)

XX DE elk.

XX KW Lambda gt11; expression vector; lambda-BI-Elk; protein tyrosine kinase;  
XX KW Elk; B1; Eph; subfamily; receptor-like tyrosine kinase; eph; eck;  
XX KW phosphorylation; phosphorylated kinase insert domain; growth factor;  
XX KW receptor kinase; platelet-derived growth factor receptor.

XX OS Rattus rattus.

XX PH Key Location/Qualifiers

FT Peptide 1..17 "Signal peptide"

FT Misc-difference 61 /note= "Cysteine residue"

FT Misc-difference 96 /note= "Cysteine residue"

FT Misc-difference 106 /note= "Cysteine residue"

FT Misc-difference 183 /note= "Cysteine residue"

FT Misc-difference 196 /note= "Cysteine residue"

FT Misc-difference 225 /note= "Cysteine residue"

FT Misc-difference 240 /note= "Cysteine residue"

FT Misc-difference 253 /note= "Cysteine residue"

FT Misc-difference 255 /note= "Cysteine residue"

FT Misc-difference 267 /note= "Cysteine residue"

FT Misc-difference 270 /note= "Cysteine residue"

FT Misc-difference 284 /note= "Cysteine residue"

FT Misc-difference 287 /note= "Cysteine residue"

FT Misc-difference 301 /note= "Cysteine residue"

FT Misc-difference 303 /note= "Cysteine residue"

FT Misc-difference 319 /note= "Cysteine residue"

FT Misc-difference 360 /note= "Cysteine residue"

FT Misc-difference 363 /note= "Cysteine residue"

FT Misc-difference 370 /note= "Cysteine residue"

FT Misc-difference 373 /note= "Cysteine residue"

FT Modified-site 425..427 /note= "N-glycosylation site"

FT Modified-site 480..482

/note= "N-glycosylation site"

CA2083521-A.

01-OCT-1993.

23-NOV-1992; 92CA-02083521.

31-MAR-1992; 92US-00861390.

(MOUN ) MOUNT SINAI HOSPITAL CORP.

Pawson A, Reedijk M, Letwin K;

WPI; 1993-406300/51.

N-PSDB; AAQ53471.

Expression of phosphorylated exogenous protein - in host cells  
transformed with two vectors, one for the protein, the other for  
catalytic domain of protein kinase.

Disclosure; Fig 3; 55pp; English.

This sequence is encoded by the elk cDNA and represents the protein  
tyrosine kinase, Elk. The Elk gene, B1, encode a protein which is a  
member of the Eph subfamily of protein tyrosine kinases. The Elk product  
is very similar to two other receptor-like tyrosine kinases, eph and eck.  
Lambda-BI-Elk may be used in the production of phosphorylated exogenous  
protein along with a further vector encoding the desired exogenous  
protein. These plasmid may be used to produce phosphorylated proteins in  
host cells which have no intrinsic capacity for phosphorylation, eg.  
bacteria. The system may be used for the expression of the phosphorylated  
kinase insert domain of a growth factor receptor kinase eg. platelet-  
derived growth factor receptor

XX Sequence 984 AA;

Query Match 75.7%; Score 3926.5; DB 2; Length 984;

Best Local Similarity 73.8%; Pred. No. 5.7e-287;

Matches 719; Conservative 128; Mismatches 126; Indels 1; Gaps 1;

Qy 11 LLLPLAAVETLMDSTTATAEGLGMVHPSPGSEVSGYDENMTTIRTYQVGVFESSON 70

Db 10 LLASAVAAMEETLMDTATAEGLGMVHPSPGSEVSGYDENMTTIRTYQVGVFESSON 69

Qy 71 NWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPGSKETFNLYYYEADSDATKTPPNW 130

Db 70 NWLTKFIRRRGAHRIHVEMKFSVRDCSSIPSPGSKETFNLYYYEADSDATKTPPNW 129

Qy 131 MENPWKVDITAADESFSQVLDLGGVRVMKINTEVRSFGPVSRSRGFYLAPODYGGMSLIIV 190

Db 130 SEAPYLKVDITAADESFSQVLDLGGVRVMKINTEVRSFGPVSRSRGFYLAPODYGGMSLIIV 189

Qy 191 RVFYKCPRIIONGAIFQETLSGAESTSLVAAGSCIANAEVDVDPKLYCNGDGEWLP 250

Db 190 RVFYKCPRIIONGAIFQETLSGAESTSLVAAGSCIANAEVDVDPKLYCNGDGEWLP 249

Qy 251 IGRMCKAGPEAVENGTVCRGCPSTFKANQGBEACTHCPINRSRTSEGATNCVCRNGYY 310

Db 250 IGRMCKAGPEAVENGTVCRGCPSTFKANQGBEACTHCPINRSRTSEGATNCVCRNGYY 308

Qy 311 RADLDPLDMPTCTTIPSAQAVISSVNETSLMLETTPRDSGGREDLVYNIICKSCSGRG 370

Db 309 RADFDPEVACTSVPSGPRNVISIVNETSIILEWPPRETGGTDDVTYNIICKCRADRR 368

Qy 371 ACTRCGDNVOYAPRQLGLTEPRYIISDLAHTQYTEIQAVNGVTDOSPPSPQFASVNIIT 430

Db 369 SCSCRDDNVFVRQLGLTECRVSIISLWHTYTFDIQAINGVSSKSPSPQFASVNIIT 428

Qy 431 TNOAAPSASVIMHOVSRTVDISITLSKSPQDPQNGVILDYELQYVEKELSYNATAIKSPT 490

Db 429 TNOAAPSASVIMHOVSRTVDISITLSKSPQDPQNGVILDYELQYVEKELSYNATAIKSPT 488

Qy 491 NTVTVQGLKAGAIYVFOVARTVAGYGRYSKMYFQMTAEAYOTSIOEKLPLIGSSAA 550  
Dy 489 NTARIDGLRPGMVVYVQVARTVAGYKFGSKMSFQTLTDDDDYKSELREQPLIAGSAA 548  
Qy 551 GLVELIAVVAIYVNCNRGPERADSEYTDKLOHYTSGHMTFPGMKIYIDPTTYEDPNEAVR 610  
Dy 549 GVVFVSLVAISVCSKRAYSKAVYSDKLQHYSTGRSGPMKIYIDPTTYEDPNEAVR 608  
Qy 611 EFAKEIDISVKIPOVITGAGFEGVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSE 670  
Dy 609 EFAKEIDVSFKIEBIVGAGEFGEVYKGLKLPKREIYVAIKTLKAGYSEKORRDLSE 668  
Qy 671 ASINGQDPHNVHLEGVTVKSTPMIITPEMENGSLDSFLRQNDGQFTVQLVGMRLGI 730  
Dy 669 ASINGQDPHNVHLEGVTVKSTPMIITPEMENGSLDSFLRQNDGQFTVQLVGMRLGI 728  
Qy 731 AAGKYLADMYVHRDLAARNILVNSLVCKVSDFLGSLFLEDDTSDPTVTSALGGKIPV 790  
Dy 729 AAGKYLSEMYVHRDLAARNILVNSLVCKVSDFLGSLFLEDDTSDPTVTSALGGKIPV 788  
Qy 791 RWTAPALQYKFTSASDWSYGIYVMEVMSYGERPYWDMNQVINAIEQDYRLPPMD 850  
Dy 789 RWTAPALQYKFTSASDWSYGIYVMEVMSYGERPYWDMNQVINAIEQDYRLPPMD 848  
Qy 851 CPSALHQLMLDCWQDRNHRKFGQIVNTLDKMRNPSNLKAMAPLSSGINLPLDRTIP 910  
Dy 849 CPALHQLMLDCWQDRNHRKFGQIVNTLDKMRNPSNLKAMAPLSSGINLPLDRTIP 908  
Qy 911 DYTSTNTVDEWLEAIKMGYKESFANAGFTSFVVSQMMEDILRLGVTLAGHOKILNS 970  
Dy 909 DYTSTNTVDEWLEAIKMGYKESFANAGFTSFVVSQMMEDILRLGVTLAGHOKILNS 968  
Qy 971 IQVRAQWQVQSV 984  
Dy 969 IHSMRVQWQVQSV 982

RESULT 16  
ADEB3382 ID ADEB3382 standard; protein; 984 AA.  
AC ADEB3382;  
XX 29-JAN-2004 (first entry)  
DE Human Protein P54762, SEQ ID NO 10976.  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX Homo sapiens.  
OS  
XX WO2003016475-A2.  
PN 27-FEB-2003.  
XX 14-AUG-2002; 2002WO-US025765.  
PF 14-AUG-2001; 2001US-0312147P.  
XX 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX (GENO) GEN HOSPITAL CORP.  
PA (FAR) BAYER AG.  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI; 2003-268312/26.  
DR GENBANK; P54762.  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.  
PS The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 984 AA;

Query Match 75.6%; Score 3924; DB 7; Length 984;  
Best Local Similarity 73.5%; Pred. No. 8.8e-287;  
Matches 720; Conservative 130; Mismatches 128; Indels 2; Gaps 2;  
Qy 1 MALRLGAALLLLPLLAAYVEETLMDSTTATAELGMMVHPSPGVEEVSVDENNTIRTYQ 60  
Dy 1 MALDYL-LULLLASAVAAMEETLMDTRTATAELGWTANPASGVEEVSVDENNTIRTYQ 59  
Qy 61 VCNVFESSQNNWLRTKFIIRRGNAHRHVMKESVRDCSSIPSPGSKCTENLYYYEADF 120  
Dy 60 VCNVFEPNQNWLTTFINRGAHRIYTEMFTVRDCSSLNPNVPGSKCTENLYYYETDS 119  
Qy 121 DSATKTFPNMNMENPVKVDITIADESFSQVDLGGVRVMKINTEVRSFGPVSRSFYLAQD 180  
Dy 120 VIATKSAFSEAPYKVDITIADESFSQVDLGGVRVMKINTEVRSFGPVSRSFYLAQD 179  
Qy 181 YGCMNSLIAVRFYRKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
Dy 180 YGACMSLLSVRFVFKCPSIVQNFVFPETMTGAESTSLVIARGTCPINAEVDVPIKLY 239  
Qy 241 CNGDGEWLPIGRCMCKAGFEAVENCTVCRGCPSTFKANQGDGDEACTHCPINRSTTSEGA 300  
Dy 240 CNGDGEWVPIGRCTCKPGYEP-ENSVACKACAPAGTFKASQEAEGCHSPNSRSPAES 298  
Qy 301 TNCVCRNGYRADLPLDMPCTTIPSAQVAVISVNETSLMLEWTPPRDGGEDILVYNI 360  
Dy 299 PICTCRGYRADFPPEVACTSVPSGPRNVISIVNETSILLEWHPPRETGGDDVTYNI 358  
Qy 361 CKSCSGRGACTRCGDNVQYAPROGLTEPRYIISDLAHTQYTEIQAINGVTPQSPF 420  
Dy 359 CKKCRADRRSCRCDDNVEFVPRQLGLTECRYSISLSLWHTPYTTFDIQAINGVSKSPF 418  
Qy 421 SPQFASVNTTNOAAPSASVIMHOVSRTVDSITLSWSQDPDPNGVILDVLOYYEKELSE 480  
Dy 419 PPOHVSVNTTNOAAPSSTVPIHQVGSATMSITLSWPEQNPQNGIILDEIRYKEHNE 478  
Qy 481 YNATAIKSPNTVTVQGLKAGAIYVFOVARTVAGYGRYSKMYFQMTAEAYOTSIOEKL 540  
Dy 479 FNSMSARSQNTARIDGLRPGMVVYVQVARTVAGYKFGSKMSFQTLTDDDDYKSELREQ 538

```
Qy 541 LPLIIGSSAAGLVFLIAVWVIAIYVNCNRGRFERADSEYDVKLQHYTSGHMTPGMKIYIDPF 600
Dy 539 LPLIAGSAAAGVFWWSILVAISIVCSRKRAYSKAVTSDKQLQHYSTGRGSPGMKIYIDPF 598
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPCKREIFVAIKTLKSGYT 660
Dy 599 TYEDPNEAVREFAKEIDISFVKIEBIVIGAGEFGEVYKGRKLPCKREIYVAIKTLKAGYS 658
Qy 661 EKQRDFLSASIMGQFDHPNVIHLEGVVTKSTPVMIIITFEMENGLSDSLRQNDGQFTV 720
Dy 659 EKQRDFLSASIMGQFDHPNIRLEGVVTKSRPVMIIITFEMENGLSDSLRQNDGQFTV 718
Qy 721 IQLVGMRLGIAAGMKYLADNMVYVHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSPTY 780
Dy 719 IQLVGMRLGIAAGMKYLAENMYVHRDLAARNILVNSNLVCKVDFGLSRVLDQDTSPTY 778
Qy 781 TSALGGKIPIRWTAPAEIAQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNOVDINAIE 840
Dy 779 TSALGGKIPVRWTAPAEIAIYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNOVDINAIE 838
Qy 841 QDYRLPPMDPCPSALHQLMLDCWQKDRNHRPKFQIIVNTLDMIRNPNLSKAMAPLSSGI 900
Dy 839 QDYRLPPMDPCPALHQLMLDCWQKDRNSRPRFAEIVNTLDMIRNPNLSKATVATITAVP 898
Qy 901 NLPLLDRTIPDYTFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTL 960
Dy 899 SQPLLDLSIPDFTFTVDDWLSAIKMWQVYRDSPLTAGFTSLQLVTQWTSDELIRIGITL 958
Qy 961 AGHOKKIILNSIQVMRAQMNQ 980
Dy 959 AGHOKKIILNSIHSRMVQISQ 978
```

## RESULT 17

ADP09563  
ID ADP09563 standard; protein; 984 AA.

XX AC ADP09563;

XX DT 12-FEB-2004 (first entry)

XX DE Human EphA1 SEQ ID NO:64.

XX KW human; protein-protein interaction; virucide; cytostatic; vaccine;

XX KW human papilloma virus; HPV; cancer.

XX OS Homo sapiens.

XX PN W02003068940-A2.

XX PD 21-AUG-2003.

XX PF 14-FEB-2003; 2003WO-US004594.

XX PR 14-FEB-2002; 2002US-0356911P.

XX PA (CURA-) CURAGEN CORP.

XX PA (HOFF ) HOFFMANN LA ROCHE INC.

XX PI Jackson A, Ooi CE, Lewin DA, Cuthill S;

XX DR WPI; 2003-689668/65.

XX DR N-PSDB; ADP09670.

XX PT New purified complex comprising a first polypeptide and a second polypeptide, useful for identifying agents for treating/preventing a condition involving altered level of the complex e.g. human papilloma virus infection, or cancer.

XX PS Example 3; SEQ ID NO 64; 156pp; English.

XX CC The invention relates to a novel purified complex comprising a first polypeptide and a second polypeptide, where the polypeptides comprise

CC defined amino acid sequences listed in the specification, and where the first polypeptide binds to the second polypeptide. A complex of the invention has virucide and cytostatic activity, and may have a use as a vaccine. The complex is useful for identifying agents for treating or preventing a conditions involving altered level of the complex, e.g. human papilloma virus (HPV) infection, or cancer. The compositions, antibodies, vectors and methods are useful for treating such diseases. CC The sequences shown in ADP09500-ADP09583 represent proteins of the CC invention.

XX SQ Sequence 984 AA;

Query Match 75.6%; Score 3924; DB 7; Length 984;

Best Local Similarity 73.5%; Pred. No. 8.8e-287;

Matches 720; Conservative 130; Mismatches 128; Indels 2; Gaps 2;

```
Qy 1 MALRRGCAALLPLLAAVEETLMDSTATAEAGVWVHPSPGSEVSGYDENMTITTYQ 60
Dy 1 MALDYL-LLLLLASA VAAAMEETLMDTRTATAEAGWTANPASGWEVSGYDENLMTITTYQ 59
Qy 61 VCNVFESSQNNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADF 120
Dy 60 VCNVFEPNQNNWLLTTFINRGAHRIYTEMFTVRDCSSLPNVPGSKETFNLYYYETDS 119
Qy 121 DSATKTFPNMNMWVKVDITIAADESFQVDLGGRVKMKINTEVRSPGVSRSFYLAQD 180
Dy 120 VIATKSAFSEAPYLVKVDITIAADESFQVDLGGRLMKVNTVRSFGPLTRNGFYLAQD 179
Qy 181 YGCMSLIAVRVFRKCPRIIONGAFOETLSGAESTSLVAARGSCIANAEVDVPTKLY 240
Dy 180 YGACMSLLSVFRVFKCPSIVQNFAPFETMTGAESTSLVIARGTCIPNAEEVDVPTKLY 239
Qy 241 CNGDGWLVPPIGRCMCKAGPEAVENGTVCRGCPSTGTFKANGQDEACTHCPINRSTTSEGA 300
Dy 240 CNGDGEMWPIGRCTCKPGYEP-ENSVACKACAGTFKASQAEAGCSCHSPNSRSPAES 298
Qy 301 TNCVCRNGYYRADLPLDMPCTTIPSAQAVISSVNETSLMLBWTTPRDSGGREDLVYNI 360
Dy 299 PICTCRGTYYRADFPPEVACTSVPSGRNVISIVNETSIILEWHPPRETGGRDVYNI 358
Qy 361 ICKSCSGRGACTCGDNQVYAPROGLTEPRIVISDLLAHTOYTRIQAVNGVTDOSPF 420
Dy 359 ICKKCRADRRSCRCDDNVEFVPRQGLTECRVVISLWHAHTPTPTDQAINGVSSKSPF 418
Qy 421 SPOFASVNTTNOAAPSAVSIMHQVSRVTDSITLSWSQDPQNGVILDYELQYKEKLESE 480
Dy 419 PPQHVSVNTTNOAAPSTVPIHQVSATMPSITLSWPEQPNGLIILDYIRIYKEHNE 478
Qy 481 YNATAIKSPNTVTVOGLKAGAIYVFQVARTVAGYRGYKGMFYQMTAEYQTSIOEK 540
Dy 479 FNSSMARSQNTNARIDCLRPGMVYVQVRAARTVAGYKFGSKMCFQTLTDDYKSELREQ 538
Qy 541 LPLIIGSSAAGLVFLIAVWVIAIYVNCNRGRFERADSEYDVKLQHYTSGHMTPGMKIYIDPF 600
Dy 539 LPLIAGSAAAGVFWWSILVAISIVCSRKRAYSKAVTSDKQLQHYSTGRGSPGMKIYIDPF 598
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPCKREIFVAIKTLKSGYT 660
Dy 599 TYEDPNEAVREFAKEIDISFVKIEBIVIGAGEFGEVYKGRKLPCKREIYVAIKTLKAGYS 658
Qy 661 EKQRDFLSASIMGQFDHPNVIHLEGVVTKSTPVMIIITFEMENGLSDSLRQNDGQFTV 720
Dy 659 EKQRDFLSASIMGQFDHPNIRLEGVVTKSRPVMIIITFEMENGLSDSLRQNDGQFTV 718
Qy 721 IQLVGMRLGIAAGMKYLADNMVYVHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSPTY 780
Dy 719 IQLVGMRLGIAAGMKYLAENMYVHRDLAARNILVNSNLVCKVDFGLSRVLDQDTSPTY 778
Qy 781 TSALGGKIPIRWTAPAEIAQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNOVDINAIE 840
Dy 779 TSALGGKIPVRWTAPAEIAIYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNOVDINAIE 838
Qy 841 QDYRLPPMDPCPSALHQLMLDCWQKDRNHRPKFQIIVNTLDMIRNPNLSKAMAPLSSGI 900
```



retinal neovascularisation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulvuary; gene therapy; vaccine.

**Homo sapiens.**

WO2003042661-A2.

22-MAY-2003.

13-NOV-2002; 2002WO-US036810.

13-NOV-2001; 2001US-0350666P.

21-NOV-2001; 2001US-0332464P;  
29-NOV-2001; 2001US-0334393P;

03-DEC-2001; 2001US-0335394P;  
14-DEC-2001; 2001US-0340376P;

08-JAN-2002; 2002US-0347Z11P;  
10-JAN-2002; 2002US-0347349P;

08-FEB-2002; 2002US-0355250P;  
13-FEB-2002; 2002US-0356714P;

20-FEB-2002; 2002US-0359077P;  
29-MAR-2002; 2002US-0368809P;

04-APR-2002; 2002US-0370110P;  
12-APR-2002; 2002US-0372246P;

05-JUN-2002; 2002US-0386614P;  
16-JUL-2002; 2002US-0396839P;

22-JUL-2002; 2002US-0397775P;  
22-JUL-2002; 2002US-0397845P;

03-SEP-2002; 200205-0409450P:

(EUSB-7) EOS BIOTECHNOLOGY INC

ALAI U, AZIZ N, GLISBURY WM  
Mack DH, Murray R, Watson S

WPI; 2003-468649/44.

N-PSDB; ADN39648.

useful for diagnosing, prognosis,

a nucleare actu III a Biologica

ACT 15273 ON 11 SEP 71 111111

whose expression is upregulated

other diseases such as angiotensin of determining the presence or

patient by detecting a nucleic acid at least 80% identical to the invention or by detecting a polypeptide of the invention. The invention or by detecting a polypeptide of the invention.

invention also relates to expression vectors and host cells for the expression of nucleic acids of the invention; antibodies which specifically bind to the nucleic acids of the invention; and methods for the detection and diagnosis of the disease.

polypeptide of the I  
and methods of screen

polypeptides and antibodies and me

cancer and other conditions such as psoriasis, ischaemia, heart disease, arteriosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularisation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.

Sequence 998 AA;

ery Match	70.7%;	Score 3670.5;	DB 7;	Length 998;
t Local Similarity	70.4%;	Prod. No. 1.2e-267;		
ches 694;	Conservative 115;	Mismatches 158;	Indels 19;	Gaps

10 UUUUUUU-----AAVEELLMDSIAIAELGLGMMVIEFSGWEEVSGIDENNNILKRIIOVCN 80  
 10 UUUUUUU-----AAVEELLMDSIAIAELGLGMMVIEFSGWEEVSGIDENNNILKRIIOVCN 81  
 23 LLLLPLLLLPGAGRALEETLMDTKWTVSELAWTSHPSGWEVSGDEAMNPRTYIOVCN 82

Qy	64	VFSSQNNWLR	TKFIRRRGAHR	IHWEMKSV	VRDCSSIPS	VPGSKCTFN	LYYYEAD	PDSA	123																																															
Db	83	VRESSQNNWLR	TGFIWRRDQRY	VYVELKFT	IRDDCN	IPNIPG	SKCTFN	LYYYEAD	142																																															
Qy	124	TKTFPNMNM	PWKVD	TIAADE	SFSDVL	GGRYVK	INTEVR	SGPVSR	SGFYLA	FODYGG	183																																													
Db	143	SASPFWM	NPYVK	VD	TIAADE	SFSD	RUDAG	----	RVNTK	VSFG	PSL	KAGFYLA	FQDQGA	198																																										
Qy	184	CMSLIAVR	PYR	KPRI	QNGAI	FOETLS	GAEST	SLVAAR	GSCIAN	AEEVD	VP	IKLYCNG	243																																											
Db	199	CMSLIS	VRAFYK	KCAST	AGTAG	FALP	PETLT	GAEP	TS	LIAP	GTCT	PNAVE	VS	VPLKLYCNG	258																																									
Qy	244	DGEWL	VP	I	GB	CM	KAG	FA	VEN	TV	CR	GPC	SFT	FKAN	QDEA	CTH	CP	INS	RT	SE	GATNC	303																																		
Db	259	DGEWM	VP	V	G	A	C	T	CAT	G	H	E	P	A	K	E	S	Q	R	C	P	P	G	S	K	A	K	Q	E	G	E	G	P	C	L	P	C	P	N	S	R	T	T	S	P	A	S	I	C	318						
Qy	304	VCNGY	VRAD	L	D	L	P	M	C	P	T	T	I	P	S	A	P	A	V	L	S	S	N	N	E	T	S	L	M	L	E	W	T	P	P	R	S	D	G	R	E	D	L	V	N	L	I	C	363							
Db	319	TCHNN	F	R	A	D	S	A	D	S	A	C	T	T	V	P	P	G	V	I	S	N	N	E	T	S	L	I	L	E	W	S	P	R	D	L	G	R	D	D	L	U	L	I	N	V	I	C	378							
Qy	364	SC	--	G	S	G	R	G	A	C	T	R	C	G	N	V	A	P	R	Q	L	G	T	E	P	R	I	Y	I	S	L	L	A	H	T	O	T	T	F	B	I	Q	A	V	N	G	T	D	O	S	P	F	S	421		
Db	379	KCHGAG	SAC	S	C	D	N	N	V	E	P	P	Q	L	G	T	E	R	R	V	H	I	S	H	L	L	A	H	T	R	T	F	E	V	Q	A	V	N	G	S	V	G	S	P	L	P	438									
Qy	422	PQFAS	V	N	I	T	N	O	A	P	S	A	V	S	I	M	H	O	V	R	T	S	I	T	S	W	S	Q	P	O	P	N	G	V	I	D	Y	E	L	O	Y	E	K	L	S	E	Y	481								
Db	439	P	R	Y	A	A	N	I	T	N	O	A	P	S	E	V	P	T	L	R	L	H	S	S	G	S	L	T	S	W	A	P	P	E	R	P	N	G	V	I	D	Y	E	M	K	Y	E	K	496							
Qy	482	NATA	I	K	S	P	T	N	T	V	T	Q	G	L	K	A	G	A	I	V	V	O	V	A	R	T	A	G	Y	G	R	Y	G	K	M	F	O	T	M	B	--	A	E	Y	T	S	I	O	E	K	540					
Db	497	I	A	S	T	V	T	S	O	M	N	S	Q	L	D	G	R	P	D	A	R	V	V	O	V	A	R	T	A	G	Y	G	O	Y	S	R	P	A	E	F	E	T	T	S	E	R	G	S	A	Q	L	O	E	K	556	
Qy	541	L	P	L	I	I	G	S	S	A	G	L	V	L	I	A	V	V	I	A	I	V	C	N	R	R	G	P	E	R	A	D	S	E	T	D	K	L	Q	H	T	S	G	H	T	P	G	M	K	I	Y	I	D	P	F	600
Db	557	L	P	L	I	V	G	S	A	T	A	G	L	V	V	A	V	V	I	A	I	V	C	L	R	K	R	H	G	S	D	S	E	V	T	E	K	L	Q	Y	---	I	A	P	G	M	K	V	I	D	P	F	612			
Qy	601	T	Y	E	D	P	N	E	A	R	E	F	A	K	E	I	D	I	S	C	K	I	E	O	V	I	G	A	G	E	F	G	E	V	C	S	H	L	K	P	G	K	E	I	F	V	A	I	K	L	S	G	Y	T		

## RESULT 20

REGOUT 20  
AAR75708

ID AAR75708 standard; protein; 973 AA.

XX

AC AAR75708;

XXE

DT 25-MAR-2003 (revised)





CC Novel EPH-related PTK cDNA clone Cek10 (given in AAQ90656) and a variant  
CC clone, Cek10+ (AAQ90658), whose product contains a 15-amino acid  
CC insertion in the juxtamembrane domain, were isolated from a chick embryo  
CC library in lambda gt11. Cek10 and Cek10+ may originate from the same gene  
CC by alternative splicing. Cek10 expression was prominent in the kidney,  
CC and to a lesser extent in the lung. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 988 AA;

Query Match 70.6%; Score 3662.5; DB 2; Length 988;  
Best Local Similarity 70.1%; Pred. No. 4.9e-267;  
Matches 684; Conservative 121; Mismatches 144; Indels 27; Gaps 5;

Qy 30 TAEIGMWHVPPSGVEEYSGVDENNTIRYQVCNVFESSQNMLRTKFIKRRGAHRIHVE 89  
Db 21 TSELATWTHETGWEYSGYDEAMNPIRTQVCNVRANQNWLRTKFIQRDVQVRYVE 80  
Qy 90 MKFSVRDCSSIPSPVSGCKTFFNLYYEADPDSATKTFPNMNMENPWVKVDTIAADESFSQ 149  
Db 81 LKFTVRDCNIGPNIPIGSKETENLFYFESDTSASANSFWMENFYIKVDTIAPDESFSK 140  
Qy 150 VDLGGRVWKNTVRSRGPVSRGFLAFODYGCMSLIARVRYFKCPRIQNGAIFQE 209  
Db 141 LESG----RVNTKVRSGFLSKNGFYLAQDLGACMSLISVRAPFYKCSNTIAGFAIFPE 196  
Qy 210 TLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGWLVPIGRCMCKAGFEAVENGTVG 269  
Db 197 TLTAETPSLVIAPGTCTPNAVEVSPLKLYCNGDGWVPGACTCAAGYEPAMKDTQC 256  
Qy 270 RGCPSGTFKANQGDCAETHCPINSRTTSEGATNCVCRNGYYRADLPLDMPCTTIPSAQ 329  
Db 257 QACPGPTFKSQGPGCPSPNPSRTTAGAATVTCICRSGPFRADADPADSACTSVPSAPR 316  
Qy 330 AVISSVNETSLMLEWTPRDSGREDLVNIIKSCSGSGRCACTRCGDNVQYAPQL--- 386  
Db 317 SVISNVNETSLVLEWSEFPDAGGRDILLNVIKCSVRRRLCSRDDNVEFVRQLGLT 376  
Qy 387 GLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFPOFASVNTTNOAPSASVSIHQVS 446  
Db 377 GLTEPRYIISKVMAHPQYTFEIQAVNGISSKSPYPHPFASVNTTNOAPSASVPTMLHS 436  
Qy 447 RTVDSITLSWSPQDPQNGVILDYELQYKE-ISEYNATAIKSPNTVTVOGLKAGAIYV 505  
Db 437 STGNSMTLSWTPPERNGIILDEYIKYSEKQGGDGIANTVTSQNSVRDLGLKANARYM 496  
Qy 506 FOVRARTVAGRYSGMYQTMTEAEYQTSIQEKLPIIGSSAAGLVFLIIVVIAIVC 565  
Db 497 VQVRARTVAGRYSLPTEPQTAAEDGSTSKTFOELPLIVGSATAGLLFVIVVIAIVC 556  
Qy 566 NRRGF-----ERADSEYTDKLQHYTSGHMTPGMKIYIDPFTYEDPNEAVR 610  
Db 557 FRKGWTEQLLSPLGRKQNSDTPETEKLOQY----VTFGKVIYIDPFTYEDPNEAVR 612  
Qy 611 EFAKEIDISCKIEQVITGAGEFVCSGHLKLPKREIFVAIKTLKSGYTEKQRDPFSE 670  
Db 613 EFAKEIDISCKIEVIGAGEFVCSGRLKLPGRREIFVAIKTLKVGYTEKQRDPFSE 672  
Qy 671 ASINGQFDHNVHLEGVWTKSTPVMIIIFEMENGLSDSLRQNDGQFTVQLVGLMGI 730  
Db 673 ASINGQFDHNIHLEGVWTKSRPVMIIIFEMENCALDSFLRLNDGQFTVQLVGLMGI 732  
Qy 731 AAGKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRFLEDDTSPTYSALGGKIPI 790  
Db 733 AAGKYLSEMYVHRDLAARNILVNSLVCKVSDFGLSRFLEDDPADPTYSALGGKIPI 792  
Qy 791 RWTAPAEIQYRKFTSASDVMSYGIWVMSYGERPVMYDMTNQDVINAIBQDYRLPPMD 850  
Db 793 RWTAPAEIAYRKFTSASDVMSYGIWVMSYGERPVMYDMNSQDVINAVEQDYRLPPMD 852  
Qy 851 CPSALHQLMDCWQDRNRHPRKFOIYNTLDKMTIRNPNSLKAMAPLSSGSLNPLDRTIP 910  
Db 853 CPTALHQLMDCWVRDRNLRPKFAQIYNTLDKLRNAASLKVIASVQSGVSGQPLDRTVP 912

Qy 911 DYTSFNTVDLWLBALIKMGQYKESFANAGFTSFVVSQMMMEDILRLGVTLAGHOKKILNS 970  
Db 913 DYTFTTTCVGMDLAIKMGYKENVVAGFASFDLVAGTAEDLLRIGVTLAGHOKKILSS 972  
Qy 971 IQVMRAQMNQIQSVEV 986  
Db 973 IQDMRLQMNQTLFVQV 988

RESULT 22  
ABU07849

ID ABU07849 standard; protein; 998 AA.

XX ABU07849;

DT 10-MAY-2003 (first entry)

DE Human ephrin receptor ligand EphB3.

XX Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;  
KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;  
KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;  
KW cell migration disorder; cell proliferation disorder; neovascularisation;  
KW ischaemia; infarction; tissue graft; transplant; human;  
KW ephrin receptor ligand; tie receptor tyrosine kinase; EphB3.

XX Homo sapiens.

XX Key Location/Qualifiers  
FT Peptide 1..33 /label= Signal\_peptide  
FT Protein 34..998 /label= Mature\_EphB3

XX W02003004529-A2.

XX 16-JAN-2003.

XX 02-JUL-2002; 2002WO-IB002524.

XX 02-JUL-2001; 2001US-0302960P.

XX (LICN ) LICENTIA LTD.

XX Alitalo K, Kubo H;

XX WPI; 2003-210341/20.

XX N-PSDB; ABX12550.

XX Identifying modulators of binding between a Tie receptor tyrosine kinase  
XX and an Ephrin ligand, useful for promoting neovascularization, comprises  
XX contacting a Tie receptor with an Ephrin in the presence of a putative  
XX modulator.

XX Disclosure; Page 142-146; 199pp; English.

XX The invention describes a method of identifying a modulator of binding  
XX between a Tie receptor tyrosine kinase and an Ephrin ligand. The method  
XX comprises contacting a Tie receptor composition with an Ephrin  
XX compound, and detecting the binding between the putative modulator  
XX in the presence and in the absence of the putative modulator. The method  
XX is useful for identifying a modulator of binding between a Tie receptor  
XX tyrosine kinase and an Ephrin ligand. Modulators identified from the  
XX method are useful in modulating angiogenic processes, including  
XX lymphangiogenesis, for treating diseases associated with aberrant Ephrin-  
XX Tie biology, aberrant growth, migration or proliferation of cells that  
XX express a Tie receptor, or for promoting growth of vessel or  
XX neovascularisation (e.g. ischaemic tissue, an infarction, a new or  
XX chronic compound, or a tissue graft or transplant). This is the amino  
XX acid sequence of human EphB3, a member of the Ephrin-B subclass of  
XX ligands that are bound to the membrane via a transmembrane domain and



SQ. Sequence 998 AA;

Query Match 70.6%; Score 3661.5; DB 7; Length 998;  
Best Local Similarity 70.2%; Pred. No. 5.9e-267;  
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

Qy 10 LLLPL-----AAVETLMDSTTATAGLGMVHPSPSGWEEVSGYDENNTIRTYQVCN 63  
Db 23 LLLPLLLPAGCRALBETLMDTKWVTSSELAWTSHPSGWEVSGYDEAMNPIRTYQVCN 82  
Qy 64 VFESSQNNWLRTKFIIRRGGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADFD 123  
Db 83 VRESSQNNWLRTKFIIRWDQVORVVELKFTVRDCNSIPNIPGCKETFNLYYYEADSDVA 142  
Qy 124 TKTPNNWENPWKVDVTIAADESPSQVDLGRVNMKINTEVRSFGFVSRSGFYLAFOQYGG 183  
Db 143 SASSPFWENPVYKVDITAPDESFRLDAG----RVNTKVSFGFLSKAGFYLAFOQGA 198  
Qy 184 CMSLIARVVRKCPRIIQAQIAPQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 243  
Db 199 CMSLISVRAFYKCASTTAGFALPETLTGAEPSTSLVAPGTCIPNAVEVSPVPLKLYCNG 258  
Qy 244 DGEWLVDIPGCMCKAGFEAVENGTVCRGSPGTGKANOQDEACTHCPINSRTTSEGATNC 303  
Db 259 DGEWVVPVGACTCATGHEPAKESQCRPCPGSYKAKQGGPCLPSPNSRTTSPAASIC 318  
Qy 304 VCRNGYYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICK 363  
Db 319 TCHNFRYADSDSADSACTVPSPPRGVINSVNETSLILEWSEPRDLGVRDLDLYNVICK 378  
Qy 364 SC--GSGRGACTRCGDNVQAPRGLUTBEPRIYISDILLAHTQYTFETQAVNGVTDQSPFS 421  
Db 379 KCHGAGGASACRCDNDVEFVPRQLGSEPRVHTSHLLAHTRYTFEYQAVNGVSGKSLP 438  
Qy 422 PQFASVNTTNOARPSAVSIMHQVSRVDSITLSWSQDOPNGVILDEYQYKEKSEY 481  
Db 439 PRVAANNTTNOAAPSEVPTLRHSSGSSLTLSWAPRPNPNGVILDEYKYEK--SEG 496  
Qy 482 NATAIKSPNTVTVOGLKAGAIYVQVARTVAGYRGYSGMYFQMTWTE-AYEQTSIQEK 540  
Db 497 IASTVTSQMSVQLDGLRPDARYVQVARTVAGYRGYSPAPETTSERGSGAQQLQEQ 556  
Qy 541 LPLIIGSAGLPLIAVVIACVNRGRFERADSEYTDKLOHTYTSGMTFGMKIYIDPF 600  
Db 557 LPLIVGSATAGLVFAVAVVIAIVCLRKQRHSGDSEYTEKLOQY----IAPGMKVYIDPF 612  
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGVCSGHLKLPGRKRIFFVAIKTKSGYT 660  
Db 613 TYEDPNEAVREFAKEIDVSCVKEIEVIGAGEFGVCRGRUKQPGRRVFAIKTKRGVT 672  
Qy 661 EKQRDFLSEASIMGQFDHPNVIHLEGVTKSTPVMITTEFMENGSLDSFLRQNDGQFTV 720  
Db 673 ERQRDFLSEASIMGQFDHPNIRLEGVTKSRPVMILTEFMENCALDSFLRNDGQFTV 732  
Qy 721 IQLVGLRGIAAGMKYLAADNMYVHRDLAARNILVNSNLCKVSDPGLSRLEDDTSDPTY 780  
Db 733 IQLVGLRGIAAGMKYLAADNMYVHRDLAARNILVNSNLCKVSDPGLSRLEDDTSDPTY 792  
Qy 781 TSALGGKIPRTWTAPEAIQVKEFTSASDVNSYGIWMEVMSYGERPYWDMTNODVINAIE 840  
Db 793 TSSLGGKIPRTWTAPEAIQVKEFTSASDVNSYGIWMEVMSYGERPYWDMTNODVINAIE 852  
Qy 841 QDRLPPLPMDCPSALHQLMDCWOKDRNHRPKFQIVNTLDMKIRNPNLSKAMAPLSSGI 900  
Db 853 QDRLPPLPMDCPTALHQLMDCWDRNDRNLAPKFSQIVNTLDMKIRNPNLSKAMAPLSSGI 912  
Qy 901 NLPLLDRTIPDYTSFNTVDWLEAIKMGQYKESFANAGFTSFDFVVSQMMEDILRLGVTL 960  
Db 913 SQPLLDRTVPTYTFTTVDWLDALIKMGYKESFVSGAFASFDLVAQMTAEDLIRIGVTL 972  
Qy 961 AGHOKKILNSIQVRAQWNIQSV 986  
Db 973 AGHOKKILSSIQDMLQWNTLPVQV 998

RESULT 24

ADD93259  
ID ADD93259 standard; protein; 998 AA.  
XX ADD93259;  
XX AC ADD93259;  
XX DT 29-JAN-2004 (first entry)  
XX DE CCMP-1.  
XX KW CCMP-1; receptor tyrosine kinase; ephrin B-type receptor 3;  
KW prostate cancer; small cell lung carcinoma; peripheral membrane;  
KW colorectal cancer; cell membrane; breast cancer; colon cancer.  
XX OS Homo sapiens.  
XX PH Key Location/Qualifiers  
XX FT Peptide 904..919  
XX FT /label= Tandem mass spectrum  
XX PN W02003087841-A2.  
XX PD 23-OCT-2003.  
XX PF 09-APR-2003; 2003WO-GB001593.  
XX PR 09-APR-2002; 2002GB-00008089.  
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX PI Boyd RS, Fletcher GC, Hudson LJ, Patel S, Terrett JA;  
XX WI; 2003-833798/77.  
XX N-PSDB; ADD93260.  
XX PT Screening for or diagnosing carcinoma in a subject or monitoring the effectiveness of carcinoma therapy by detecting and/or quantifying in a biological sample obtained from the subject a CCMP-1 polypeptide or a nucleic acid molecule.  
XX PS Claim 1; Fig 1; 62pp; English.  
XX CC This sequence represents the CCMP-1 protein, which is a receptor tyrosine kinase also known as ephrin B-type receptor 3. CCMP-1 is one of 15 genes overexpressed in prostate cancer tissue, and has also been found at moderate to low levels in three out of four small cell lung carcinoma cell lines. CCMP-1 is localised to the peripheral membrane. It was isolated from colorectal cancer cell membranes and breast cancer cell membranes, purified by 1D gel electrophoresis and characterised by mass spectrometry before being cloned. CCMP-1 may be used in the method of the invention for screening for and/or diagnosing carcinoma in a subject and/or monitoring the effectiveness of carcinoma therapy. The method comprises detecting and/or quantifying in a biological sample obtained from the subject, a CCMP-1 polypeptide or a nucleic acid molecule. The CCMP-1 polypeptide, the nucleic acid molecule, an antibody or agent which interacts with, or modulates the expression or activity of a CCMP-1 polypeptide or the expression of a CCMP-1 nucleic acid, is useful in the manufacture of a medicament for treating or preventing carcinoma, e.g., breast cancer or colon cancer.

SQ Sequence 998 AA;

Query Match 70.6%; Score 3661.5; DB 7; Length 998;  
Best Local Similarity 70.2%; Pred. No. 5.9e-267;  
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

Qy 10 LLLPL-----AAVETLMDSTTATAGLGMVHPSPSGWEEVSGYDENNTIRTYQVCN 63  
Db 23 LLLPLLLPAGCRALBETLMDTKWVTSSELAWTSHPSGWEVSGYDEAMNPIRTYQVCN 82  
Qy 64 VFESSQNNWLRTKFIIRRGGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADFD 123

Db	83	VRESSQNNWLR7GFIWRDQVQVVYELKFTVRDCNSIPNTPGSKXTFNLFFYEADSDVA	142
Qy	124	TKTFENWENPMVKYDITIAADESFQVDLGRVMKINTEVRSFGPVSRSQGYLAFODYGG	183
Db	143	SASSFFWENPMVKYDITIAADESFQVDLGRVMKINTEVRSFGPVSRSQGYLAFODYGG	198
Qy	184	CMSLIAVRVFKRCPRIIONGAIFQETLSGABESTSLVAARGSCIANAEVDVPIKLYCNG	243
Db	199	CMSLISVRAFYKKCASTTAGFALPETLTGAEPSTSLVAPGTCIPNAVEVSPLKLYCNG	258
Qy	244	DGEWLVPTRCMCKAGFAVENGTVCRCPSGTFKANOGDEACTHCPINSRSTSGATNC	303
Db	259	DGEWMPVPGACTCATGHEPAAKESQCRPCPGSKYAKQGGPCCLPCPPNSRSTSPAASITC	318
Qy	304	VCRNGYIRADLDPLDMPCTTIPSAQOAVISSVNETSLMELWTPPRDSQGREDIIVNIICK	363
Db	319	TCHNNFYRADSADSACTTVPSPRGVISNVNETSLLEWSEPRDLGVDRDLLYNVICK	378
Qy	364	SC--GGRGACTRCGDNVOYAPROGLTEPRIYISDILLAHTQYTFEIQAVNGVTDOSPFS	421
Db	379	KCHGAGGASACRCDNVEFPROGLSEPRVHTSHLLAHTRYTFEYQAVNGVSGKSLP	438
Qy	422	POFASVNIITNQAAPSANSIMHQSRTVDSTITLSWSOPDOPNGVILDYELQYKEKLSY	481
Db	439	PRYAANIITNQAASEVPTLURLSHSSGSSUTLSWAPPENGVILDYEMKFEK--SGS	496
Qy	482	NATAIKSPNTVTVOGLKAGAIYFQVRAARTVAGYGRYSKMVFQNTME--AEYQTSIQBK	540
Db	497	IASTVTSQMNVSQOLGRLPDARYVQVRAARTVAGYGRYSKPAEFETTSERGSAQOLQBO	556
Qy	541	LPILITSSAAGLVFLIAVVVIAIACNRGRFPEADSEYTDKLOHTSGHMTPGMKIYIDPF	600
Db	557	LPLIVGSAVAGLVFVVAVVIAIACLRQKRGSDSEYTEKLQOY---IAPGMKVYIDPF	612
Qy	601	TYEDPNEAREFAKIDISCVKIEOVIGAGFEGVCGSHLKLPOKRIEFAIKTLKSGYT	660
Db	613	TYEDPNEAREFAKIDISCVKIEOVIGAGFEGVCGSHLKLPOKRIEFAIKTLKSGYT	672
Qy	661	EKORRDLSEASIMGQFDPHPNVIHLEGVYVTKSTPMIITEFMENGLSDSLRQNDQOFTV	720
Db	673	ERQRRDLSEASIMGQFDPHPNVIHLEGVYVTKSTPMIITEFMENGLSDSLRQNDQOFTV	732
Qy	721	IQLVGLMRGIAAGMKYLADNVYHRDLAARNILVNSNLCKVSDPGLSRLEDDTSDPTY	780
Db	733	IQLVGLMRGIAAGMKYLSMNYYHRDLAARNILVNSNLCKVSDPGLSRLEDDTSDPTY	792
Qy	781	TSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGYVMWEVMSYGERPMDTNDQVINAIE	840
Db	793	TSSLGGKIPIRWTAPEAIQYRKFTSASDVMSYGYVMWEVMSYGERPMDTNDQVINAIE	852
Qy	841	QDYRLPPPPMDCPSALHQLMLDCWKQKDRNHRPKFOIVNTLDKMTIRNPSIKAMAPISSGI	900
Db	853	QDYRLPPPPMDCPSALHQLMLDCWKQKDRNHRPKFOIVNTLDKMTIRNPSIKAMAPISSGI	912
Qy	901	NLPLLDRTIPDYTSFNTVDWELEATKMGQYKESFANAGFTSFDDVVVSQMMMEDILRLGVTL	960
Db	913	SQPLLDRTIPDYTSFNTVDWELEATKMGQYKESFANAGFTSFDDVVVSQMMMEDILRLGVTL	972
Qy	961	AGHQKILANSIQVMRAQNNQIOSVEV	986
Db	973	AGHQKILANSIQVMRAQNNQIOSVEV	998

RESULT 25  
ADQ20030  
ID ADQ20030 standard; protein; 998 AA.

XX  
DT 26-AUG-2004 (first entry)

XX DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2850.

soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.  
Homo sapiens.  
WO2004048938-A2.  
10-JUN-2004.  
26-NOV-2003; 2003WO-US038193.  
26-NOV-2002; 2002US-0429739P.  
(PROT-) PROTEIN DESIGN LABS INC.  
Aziz N, Ginsburg WM, Zlotnik A;  
WPI; 2004-441208/41.  
Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

RESULT 25

ADQ20030

ID ADO20030 standard; protein; 998 AA.

XX  
T  
ADQZ

AC ADQ20030;

XX

DT 26-AUG-2004 (first entry)

XX

DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2850.





Db 605 TYEDPNEAVREFAKEIDVSCVKIEBIVGAGEFGEVCRGLKQPGRRVFAIKTLKVGYT 664  
 Qy 661 EKQRDFLSASIMQGFDPHNVHLEGVVTKSTPVMIIITFPMENGSLDSFLRNDGQFTV 720  
 Db 665 ERQRDFLSASIMQGFDPHNVHLEGVVTKSTPVMIIITFPMENGSLDSFLRNDGQFTV 724  
 Qy 721 IQLVGLRGIAAGMKYLADNMVYHRLAARNILVNSLVCKVDFGLSRELEDDTSPTY 780  
 Db 725 IQLVGLRGIAAGMKYLSEMMYVHRLAARNILVNSLVCKVDFGLSRELEDDTSPTY 784  
 Qy 781 TSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWMTNQDVINAIE 840  
 Db 785 TSSLGKIPRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWMTNQDVINAIE 844  
 Qy 841 QDYRLPPMPCPSALHOLMDCWOKDRNHRPKFQIIVNTLDKMRNPSNKKAMAPLSSGI 900  
 Db 845 QDYRLPPMPCPSALHOLMDCWDRNHRPKFQIIVNTLDKMRNPSNKKAMAPLSSGI 904  
 Qy 901 NLPLDRTIPTYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTL 960  
 Db 905 SQPLDRTVPTYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGVTL 964  
 Qy 961 AGHOKILNSIQVRAQNMNQIQSV 986  
 Db 965 AGHOKILNSIQVRAQNMNQIQSV 990

## RESULT 28

AAR75843  
 ID AAR75843 standard; protein; 993 AA.

XX AAR75843;

AC AAR75843;

DT 25-MAR-2003 (revised)

DT 24-NOV-1995 (first entry)

XX Protein p140 cDNA from rat skeletal muscle myoblast cell line L6.

XX Protein p140; insulin; tyrosine phosphorylation.

XX Rattus rattus.

XX EF659883-A2.

XX 28-JUN-1995.

XX 24-NOV-1994; 94EP-00118524.

XX 24-NOV-1993; 93JP-00315806.

XX (ONOY ) ONO PHARM CO LTD.

XX Tajima H, Kitagawa K, Ohno H;

XX WPI; 1995-226291/30.

XX Isolated protein p140 polypeptide - and treatment of diabetes based on

XX tyrosine phosphorylation of protein p140.

XX Claim 1; Page 19-23; 42pp; English.

XX A cDNA library was established from rat skeletal myoblast cell line L6.

XX DNA fragments of approx. 400 bp were recovered and subjected to cloning.

XX 20 plasmids were sequenced. Sequence data of cDNA fragments were

XX constructed to the linkage sequences with the DNA programme DNASIS. The

XX basic sequence protracted in AAQ90972 was hence constructed. From sequence

XX data of the whole cDNA length, the ORF was determined. The AA sequence

XX was further translated and the sequence thus established is illustrated

XX in AAR75843. One of the frames possesses the 2993-bp ORF, that was

XX approximated to 3000 bp of the whole ORF length of the Eck family. p140

XX is used for the prevention and treatment of diabetes. Dosage is 10 microg

XX -1000 mg (p.o.) or 10 microg-100mg (i.v.). (Updated on 25-MAR-2003 to

CC correct PN field.)

SQ Sequence 993 AA;

Query Match 69.5%; Score 3603.5; DB 2; Length 993;

Best Local Similarity 68.5%; Pred. No. 1.4e-262;

Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;

Qy 17 AAVEETILMDSTTATA-----ELGMVHPHPPSGWEEVSGYDENMNTRTY 59  
 Db 11 AAARAAEAATNSLSILVRPTSGSRIDSEFVELAWTSHFESGWEEVSADEANMPTTY 70  
 Qy 60 QVCNVFESSQNNWLRTKFIIRRGARHIVHEKFSVRDCSSIPSPGSKCTFNLYYEAD 119  
 Db 71 QVCNVFESSQNNWLRTKFIIRRGARHIVHEKFSVRDCSSIPSPGSKCTFNLYYEAD 130  
 Qy 120 FDSATKTFNNMNPVWVKTIIAADRSFSQVDLGGVRMKINTVRSRSGPVSRSGFYLAQ 179  
 Db 131 SDVASASSPPFMMNPVWVKTIIAADRSFSQVDLGGVRMKINTVRSRSGPVSRSGFYLAQ 186  
 Qy 180 DYGGCKSLIAVRVYRKCPRIIQNGAIFQETLGAESTLSVAARGSCIANAEVDVPIKL 239  
 Db 187 DQACMSLSIVRAFYKCASTTAGFALFPTLTGAEPTSLVIAPGTCIANA VESVPLKL 246  
 Qy 240 YCNGDGEWLPIGRCMCKAGFEAVENGTVCRGCPGTFKANOQDEACTHCPIINSRTTSEG 299  
 Db 247 YCNGDGEWLPIGRCMCKAGFEAVENGTVCRGCPGTFKANOQDEACTHCPIINSRTTSPA 306  
 Qy 300 ATNCVCNGYIRADLPDLPCTTIIPSAPOAVISSVNETSILMLEWTPPRSGREDLVYN 359  
 Db 307 ASICTCHNNFYRADSDTADSACTTVPSPRGVSNVNETSILILEWSEPRDLGCRDDLLYN 366  
 Qy 360 IICKSGSGRGA-----CTRCGNVOYAPRQLGTETPIYISDLAHTQVTFEIQAVNGV 414  
 Db 367 VICCKRGSGAGGATCSCDDNVEFEPRLGLTERVHSHLLAHTRTFEVQAVNGV 426  
 Qy 415 TDQSPSPQFASVNTTNAAPSASIMQVSRVDSITLSWSQDPQNGVILDYEIQY 474  
 Db 427 SGKSPLPYAAVNTTNAAPSASIMQVSRVDSITLSWSQDPQNGVILDYEIQY 486  
 Qy 475 EKSLSEYNATAIKSPNTVTVOGLKAGAIYVFOVARTVAGYGRYSKMYFOIWMTE-AEY 533  
 Db 487 EK--SKGIASVTVSQKNSVQLDGLQPDARYVVOVARTVAGYGRYSKMYFOIWMTE-AEY 544  
 Qy 534 QTSIQEKLPLIIIGSSAAGLVFLIAVVVIAIVCNRRGPERADSEYTDKLOHYTSGHMTPCM 593  
 Db 545 AQQLQQLPLIVGSTVAGFVFWVWVIALVCLRKORQGPDAEYTEKLQY----VAPRM 600  
 Qy 594 KIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRREIFVAIK 653  
 Db 601 KVIIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRREIFVAIK 660  
 Qy 654 TLKSGYTEKORRDFLSEASIMQGFDPHNVHLEGVVTKSTPVMIIITFPMENGSLDSFLRQ 713  
 Db 661 TLKVGYTEKORRDFLSEASIMQGFDPHNVHLEGVVTKSTPVMIIITFPMENGSLDSFLRL 720  
 Qy 714 NDCQFTVQLVGLRGIAAGMKYLADNMVYHRLAARNILVNSLVCKVDFGLSRELEDD 773  
 Db 721 NDCQFTVQLVGLRGIAAGMKYLSEMMYVHRLAARNILVNSLVCKVDFGLSRELEDD 780  
 Qy 774 DTSPTYTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWMTNQ 833  
 Db 781 DTSPTYTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWMTNQ 840  
 Qy 834 DVINAIEQYRLPMPMDPSALHOLMDCWOKDRNHRPKFQIIVNTLDKMRNPSNKKAM 893  
 Db 841 DVINAIEQYRLPMPMDPSALHOLMDCWOKDRNHRPKFQIIVNTLDKMRNPSNKKAM 900  
 Qy 894 APLSSGILNPLDRTIPTYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDI 953  
 Db 901 ASAPSQMSQLDRTVPTYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDI 960  
 Qy 954 LRLGVTLAGHOKILNSIQVRAQNMNQIQSV 986









**This Page Blank (usp10)**



## ALIGNMENTS

## RESULT 1

I78842  
receptor protein-tyrosine kinase - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 18-Jun-1999  
C;Accession: I78842  
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995  
A;Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty A;Reference number: I58351; MUID:95206782; PMID:7898931  
A;Accession: I78842  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-970 <RES>  
A;Cross-references: GB:L36643; NID:g551609; PID:AAA74244.1; PID:g551610  
C;Genetics:  
A;Gene: HEK5  
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h F;603-871/Domain: protein kinase homology <KIN>  
F;894-960/Domain: SAM homology <SAM>

Query Match 98.1%; Score 5089; DB 2; Length 970;  
Best Local Similarity 99.4%; Pred. No. 2.7e-225;  
Matches 966; Conservative 2; Mismatches 2; Indels 2; Gaps 1;  
Qy 15 LLAVESTLMDSTTATAELGVMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQNNWLR 74  
Db 1 LLAVESTLMDSTTATAELGVMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQNNWLR 60  
Qy 75 TKTRRRGAHRIHVMKFSVRDCCSIPSPGCKETENLYVYADPDSATKTPNNMENP 134  
Db 61 TKTRRRGAHRIHVMKFSVRDCCSIPSPGCKETENLYVYADPDSATKTPNNMENP 120  
Qy 135 WKVVDTTAADESFSQVDLGRVVKINTEVRSGFVSRGFLAFQDYGGCWSLIAVRVY 194  
Db 121 WKVVDTTAADESFSQVDLGRVVKINTEVRSGFVSRGFLAFQDYGGCWSLIAVRVY 180  
Qy 195 RKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRC 254  
Db 181 RKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRC 240  
Qy 255 MCKAGFEAVNGTVCRCPGSGTFRKANGDDEACTHCPINSTRTTSEGNATNCVCRNGYRADL 314  
Db 241 MCKAGFEAVNGTVCRCPGSGTFRKANGDDEACTHCPINSTRTTSEGNATNCVCRNGYRADL 300  
Qy 315 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 374  
Db 301 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 360  
Qy 375 CGDNVQVAPRQLGTEPRYISDLAHTQYTFEIQAVNGVTDQSPFPQASVNIITNQ 434  
Db 361 CGDNVQVAPRQLGTEPRYISDLAHTQYTFEIQAVNGVTDQSPFPQASVNIITNQ 420  
Qy 435 APSAVSIHQVSRVDSITLSWSQDPNGVILDYQYKEKSEYNATAIKSPNTVT 494  
Db 421 APSAVSIHQVSRVDSITLSWSQDPNGVILDYQYKEKSEYNATAIKSPNTVT 480  
Qy 495 VQGLKAGAIYVQVRAARTVAGYGRYSGKMFQTMTEAEYQTSIOEKLPLIIGSSAAGLVF 554  
Db 481 --GLKAGAIYVQVRAARTVAGYGRYSGKMFQTMTEAEYQTSIOEKLPLIIGSSAAGLVF 538  
Qy 555 LIAVWVIAVCNRRGFPRADSEYTDKLOHTYSGHMTFGMKIYIDPFYEDPNEAVREFAK 614  
Db 539 LIAVWVIAVCNRRGFPRADSEYTDKLOHTYSGHMTFGMKIYIDPFYEDPNEAVREFAK 598  
Qy 615 EIDIISCVKIEQVIGAGFGEVCSGHLKIPGKREIFVAIKTLKSYTEKQRDRDFLSEASIM 674  
Db 599 EIDIISCVKIEQVIGAGFGEVCSGHLKIPGKREIFVAIKTLKSYTEKQRDRDFLSEASIM 658  
Qy 675 GQFDHPNVIHLEGVVTKSTPYMIITFPMENGLSDSLRQNDGQFTVIQLVGLMLRGAAGM 734

## RESULT 2

A56599  
embryo kinase 5 - chicken  
N;Alternate names: receptor tyrosine kinase Cek5  
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C;Species: Gallus gallus (chicken)  
C;Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 04-Feb-2000  
C;Accession: A56599  
R;Pasquale, E.B.  
Cell Regul. 2, 523-534, 1991  
A;Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor A;Reference number: A56599; MUID:92144672; PMID:1664238  
A;Accession: A56599  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-995 <PAS>  
A;Cross-references: GB:M62325; NID:g211448; PID:AAA48667.1; PID:g211449  
A;Note: sequence extracted from NCBI backbone (NCBIN:81999, NCBI:P:82001)  
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kin F;628-896/Domain: protein kinase homology <KIN>  
F;836-844/Region: protein kinase ATP-binding motif  
F;919-985/Domain: SAM homology <SAM>

Query Match 96.3%; Score 4993.5; DB 2; Length 995;  
Best Local Similarity 95.8%; Pred. No. 6.5e-221;  
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;  
Qy 10 LLLPLLAVEETLMDSTTATAELGVMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQ 69  
Db 18 LALLPLLAVEETLMDSTTATAELGVMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQ 77  
Qy 70 NNWLRTKTRRRGAHRIHVMKFSVRDCCSIPSPGCKETENLYVYADPDSATKTFPN 129  
Db 78 NNWLRTKTRRRGAHRIHVMKFSVRDCCSIPSPGCKETENLYVYDESDFDSATKTFPN 137  
Qy 130 WMENPMVKVDTTIAADESFSQVDLGRVVKINTEVRSGFVSRGFLAFQDYGGCWSLIA 189  
Db 138 WMENPMVKVDTTIAADESFSQVDLGRVVKINTEVRSGFVSRGFLAFQDYGGCWSLIA 197  
Qy 190 VRVYRKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 249  
Db 198 VRVYRKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 257  
Qy 250 PIQRCMCKAGFEAVNGTVCRCPGSGTFRKANGDDEACTHCPINSTRTTSEGNATNCVCRNGY 309  
Db 258 PIQRCMCKAGFEAVNGTVCRCPGSGTFRKANGDDEACTHCPINSTRTTSEGNATNCVCRNGY 317  
Qy 310 YRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGR 369

Db 318 YRADADPDMPTTIPSAQAVISVNETSLMELTWTTPRSGGREDIVYNIICKSCGSGR 377  
Qy 370 GACTRCGDNVQYAPROGLGLETPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 429  
Db 378 GACTRCGDNVQYAPROGLGLETPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 437  
Qy 430 TTNOAAPSASVIMHQVSRVTDSITLSWSQDPQNGVILDYELQYKEKSEYNATAIKSP 489  
Db 438 TTNOAAPSASVIMHQVSRVTDSITLSWSQDPQNGVILDYELQYKEKSEYNATAIKSP 497  
Qy 490 TMTVVOGLKAGAIYVQVRAARTVAGYGRYSGKMYFQMTAEAEYQTSIQKPLIIGSSA 549  
Db 498 TMTVVOGLKAGAIYVQVRAARTVAGYGRYSGKMYFQMTAEAEYQTSIQKPLIIGSSA 557  
Qy 550 AGLVFLAVVIAIVCN- RGFERADSEYTDKLOHTYSGHMTGPKMKIYIDPFTVEDPNEA 608  
Db 558 AGLVFLAVVIAIVCN- RGFERADSEYTDKLOHTYSGHMTGPKMKIYIDPFTVEDPNEA 617  
Qy 609 VREPAKEIDISCVKIEQVIGAGFGRVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDPL 668  
Db 618 VREPAKEIDISCVKIEQVIGAGFGRVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDPL 677  
Qy 669 SEASIMQFDPHPNVHLEGVVTKSTPVMIIITFPNENGSLDSFLRQNDGQFTVQLVGMRL 728  
Db 678 SEASIMQFDPHPNVHLEGVVTKSTPVMIIITFPNENGSLDSFLRQNDGQFTVQLVGMRL 737  
Qy 729 GIAAGMKYLDAMNVVHRDLAARNILVNSNLVCKVDSDFGLSRFLRDEDDTSDPTYSALGKI 788  
Db 738 GIAAGMKYLDAMNVVHRDLAARNILVNSNLVCKVDSDFGLSRFLRDEDDTSDPTYSALGKI 797  
Qy 789 PIRWTAPEAIQYRKFTSASDVMSYGIYVWVMSYGERPYMDMTNQDVINAIEQDYRLPPP 848  
Db 798 PIRWTAPEAIQYRKFTSASDVMSYGIYVWVMSYGERPYMDMTNQDVINAIEQDYRLPPP 857  
Qy 849 MDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMIENPNSLKAMAPLSSGINLPILDR 908  
Db 858 MDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMIENPNSLKAMAPLSSGINLPILDR 917  
Qy 909 IPDVTSTNTDWELEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGHOKKIL 968  
Db 918 IPDVTSTNTDWELEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGHOKKIL 977  
Qy 969 NSIQVMEARQNNQIQSVEV 986  
Db 978 NSIQVMEARQNNQIQSVEV 995

## RESULT 3

A39753  
protein-tyrosine kinase (EC 2.7.1.112) elk precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 09-Jul-2004  
C:Accession: A39753; S04327  
R:Lhotak, V.; Greer, P.; Letwin, K.; Pawson, T.  
Mol. Cell. Biol. 11, 2496-2502, 1991  
A:Title: Characterization of elk, a brain-specific receptor tyrosine kinase.  
A:Reference number: A39753; MUID:91203869; PMID:2017163  
A:Accession: A39753  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-984 <LHO>  
A:Cross-references: UNIPROT:P09759; GB:M59814  
R:Letwin, K.; Yee, S. P.; Pawson, T.  
Oncogene 3, 621-627, 1988  
A:Title: Novel protein-tyrosine kinase cDNAs related to fps/fes and eph cloned using anti-  
A:Reference number: S04327; MUID:94167102; PMID:2485255  
A:Accession: S04327  
A:Molecule type: mRNA  
A:Residues: 605-984 <LET>  
A:Cross-references: EMBL:X13411; NID:g56094; PIDN:CAA31777.1; PID:g56095  
C:Genetics:  
A:Gene: elk

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat he  
C:Keywords: ATP; autophosphorylation; kinase-related transforming protein; phosphoprotein  
F:617-885/Domain: protein kinase homology <KIN>  
F:625-633/Region: protein kinase ATP-binding motif  
F:908-974/Domain: SAM homology <SAM>

Query Match 75.8%; Score 3934.5; DB 2; Length 984;  
Best Local Similarity 73.9%; Pred. No. 1.5e-172;  
Matches 720; Conservative 128; Mismatches 125; Indels 1; Gaps 1;  
Qy 11 LLLPLAAVEETLMDSTTAELGMMVHPSPSGVEEYGDENMNTIRTYQVNCVFESSQ 70  
Db 10 LLASAAVEETLMDSTTAELGMMVHPSPSGVEEYGDENMNTIRTYQVNCVFESSQ 69  
Qy 71 NWLRTFIRRGGAHRHVENKFSVRDCSSIPSPVSGCKETFNLYYYEADDSATKTPNW 130  
Db 70 NWLRTFIRRGGAHRHVENKFSVRDCSSIPSPVSGCKETFNLYYYEADDSATKTPNW 129  
Qy 131 MENPWKVDITAADESPQVDLGGVRVMKINTEVRSPGVSRSFYLAQYGGCMSLIIV 190  
Db 130 SEAPYLKVDITAADESPQVDLGGVRVMKINTEVRSPGVSRSFYLAQYGGCMSLIIV 189  
Qy 191 RVFVRKCPRIIONGAIQFETLSGABSTSLVAARSGCIANAEEVDVPIKLYCNGDGEWLP 250  
Db 190 RVFVRKCPRIIONGAIQFETLSGABSTSLVAARSGCIANAEEVDVPIKLYCNGDGEWLP 249  
Qy 251 IGRCMKAGPEAVENGTVCRGCPSTFKANQGBEACTHCPINSGRTTSEGATNCVCRNGY 310  
Db 250 IGRCTCKAGYEP-ENSVACKACAGATFKASQEAEGCSHCPSNSRSPSEASPICTCRGY 308  
Qy 311 RADLDPLDMPCTTIPSAQAVISVNETSLMELTWTTPRSGGREDIVYNIICKSCGSGR 370  
Db 309 RADFDPEVACTSPVSGPRNVSIVNETSIILEWHPPRETGRDQDVYNIICKCRADR 368  
Qy 371 ACTRCGDNVQYAPROGLGLETPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 430  
Db 369 SCRCDDNVFVRPQGLTECRVSIISLWHTPTFDIQAINGVSSKPPPPQHVSNIT 428  
Qy 431 TNOAAPSASVIMHQVSRVTDSITLSWSQDPQNGVILDYELQYKEKSEYNATAIKSP 490  
Db 429 TNOAAPSASVIMHQVSRVTDSITLSWSQDPQNGVILDYELQYKEKSEYNATAIKSP 488  
Qy 491 NTVTVOGLKAGAIYVQVRAARTVAGYGRYSGKMYFQMTAEAEYQTSIQKPLIIGSSA 550  
Db 489 NTARIDGLRPGMVVQVRAARTVAGYGRYSGKMYFQMTAEAEYQTSIQKPLIIGSSA 548  
Qy 551 GLVFLAVVIAIVCN- RGFERADSEYTDKLOHTYSGHMTGPKMKIYIDPFTVEDPNEAVR 610  
Db 549 GVVFVWSLVSAISIVCSKRAYSKEAVYSDKLQHYSTGRSGPMKIYIDPFTVEDPNEAVR 608  
Qy 611 EFAKEIDISCVKIEQVIGAGFGRVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDPLSE 670  
Db 609 EFAKEIDISCVKIEQVIGAGFGRVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDPLSE 668  
Qy 671 ASIMGQFDPHPNVHLEGVVTKSTPVMIIITFPNENGSLDSFLRQNDGQFTVQLVGMRLGI 730  
Db 669 ASIMGQFDPHPNVHLEGVVTKSTPVMIIITFPNENGSLDSFLRQNDGQFTVQLVGMRLGI 728  
Qy 731 AAGMKYLDAMNVVHRDLAARNILVNSNLVCKVDSDFGLSRFLRDEDDTSDPTYSALGKIPI 790  
Db 729 AAGMKYLDAMNVVHRDLAARNILVNSNLVCKVDSDFGLSRFLRDEDDTSDPTYSALGKIPI 788  
Qy 791 RWTAPAEAIQYRKFTSASDVMSYGIYVWVMSYGERPYMDMTNQDVINAIEQDYRLPPPMD 850  
Db 789 RWTAPAEAIQYRKFTSASDVMSYGIYVWVMSYGERPYMDMTNQDVINAIEQDYRLPPPMD 848  
Qy 851 CPSALHQLMDCQKDRNHRPKFGQIVNTLDKMIENPNSLKAMAPLSSGINLPILDR 910  
Db 849 CPSALHQLMDCQKDRNHRPKFGQIVNTLDKMIENPNSLKAMAPLSSGINLPILDR 908  
Qy 911 DYTSTNTDWELEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGHOKKILNS 970  
Db 909 DYTSTNTDWELEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGHOKKILNS 968

```
QY 971 IQWRAQMNQIQSV 984
Db 969 IHSMRVQMNSPSV 982

RESULT 4
151672
receptor tyrosine kinase - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51672
R:Jones, T.L.; Karavanova, I.; Maeno, M.; Ong, R.C.; Kung, H.F.; Daar, I.O.
Oncogene 10, 1111-1117, 1995
A:Title: Expression of an amphibian homolog of the Eph family of receptor tyrosine kinases
A:Reference number: I51672; MUID:95215070; PMID:7700636
A:Accession: I51672
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-985 <JON>
A:Cross-references: UNIPROT:Q91571; EMBL:U14164; NID:9557214; PIDN:AAA74888.1; PID:99572
C:Gene: XEK
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: Atp; transmembrane protein
F:618-886/Domain: protein kinase homology <KIN>
F:626-634/Region: protein kinase ATP-binding motif
F:909-975/Domain: SAM homology <SAM>

Query Match 72.6%; Score 3767; DB 2; Length 985;
Best Local Similarity 71.2%; Pred. No. 6.6e-165;
Matches 699; Conservative 131; Mismatches 140; Indels 12; Gaps 5;

QY 6 LGALLLLPL-----LAAVEETLMDSTTATAELGWMVHPSPGSEVSGYDENMTIRYQV 61
Db 3 LNVLLLLCLSGGQVGAEEETLMDTRTATALGTWANTPSSGSEVSGYDENMTIRYQV 62
QY 62 CNVFESSONNWLRTKFIIRRGARHIVEMKFSVDCSSIPSPGSCKETFNLYYYEADFD 121
Db 63 CNVGPQKNWLLTTFIPRGARHVVYEMRTVDCSSLPNVPSCKETFNLYYYEADSN 122
QY 122 SATKTFPNNMENPVKVDITIAADESFSQVDLGGRWKINTEVRSFGVSRSGFLAPQDY 181
Db 123 IENKISTFWNESPLKVDITIAADESFSQVDLGGRWKINTEVRSFGFLTRSGFLAPQDY 182
QY 182 GCGSLIAVRVYFKCPRIIQNGAIFQTLGSAESTSLVAARGSCIANAEVDVPIKLYC 241
Db 183 GACMELLSVRVFFKEMPSVQVQLLVFPETMTGAESTSLVIARGTCIPNAEEVDVPIKLYC 242
QY 242 NGDGEWLVPIGRCMKAGFEAVENGTVCRGCPSGTFFKANQGDGDEACTHCPINSRTTSGAT 301
Db 243 NGDGEWVVPIGKCTCKAGYEP-ENHVCKACPAAMFKANQGMGICACQCPANSRSTSEASP 301
QY 302 NCVCRNGYRADLPLDMPCTTIPAPQAVTSVNNTSLMEWPPRDSGGREDLVNII 361
Db 302 ICICRNGYRADFDTPAECTSVPSGPRNVIISVNETAITLEWPPRDTGRDDVDNIV 361
QY 362 CKSCGSGRGACRCDGNDVQAPROLGLTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFS 421
Db 362 CKKCRADRCACRCDNDVDFVROLGLTDRVFIENLWHTPYTFETQAVNGVINKSPFP 421
QY 422 PQFASVNTTNOAAPSAVSIMHQVSRVDSITLWSQDPQNGVILDYELQYKEKSEY 481
Db 422 PQHVSNTTNOAAPSSVPIHQVKATMKSITLSPQEQEPNGIILDEIYRYEKDHFEF 481
QY 482 NATATKSPNTVTVOGLKAGALYVE---QVRARTVAGYGRYSGKMYFOTMTAEAYQTSIQ 538
Db 482 NSSLSARQNTARRTG---GRVFMFMSVQVRARTVAGYGRYSGKMYFOTMTAEAYQTSIQ 538
QY 539 EKPLPIIGSAAAGLVIAVAVIAVCNRRGPERADSEYTKLQHYTSGHMTPGMKIYID 598
Db 539 EQLPL-TGSAAGVGVFIVSLVAISIVCSRKRYSKEAVYSDKLQHYSTGRSGPGMKIYID 597
```

```
QY 599 PFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSHLKLPGRKEIFVAIKTLKSG 658
Db 598 PFTYEDPNEAVREFAKEIDVSVFKIEEVIGAGEFGEVYKGRKLPKRSREISVAIKTLKAG 657
QY 659 YTEKQRDRFLSEASTMGOFDHPNVHLGVTGKTPVMIITEFMENGLSDFLRQNDQGF 718
Db 658 YSEKQRDRFLSEASTMGOFDHPNIIIRLEGVTKSRPVMIIITEFMENGLSDFLRQNDQGF 717
QY 719 TVIQLVGLMRLGIAGMKYLAADNMYVHRDLAARNLVNSNLVCKYDSDFGLSRFLBDDTSDP 778
Db 718 TVIQLVGLMRLGIAGMKYLSWNVVHRDLAARNLVNSNLVCKYDSDFGLSRFLBDDTSDP 777
QY 779 TVTSALGOKIPIRWTAPPAIQAIRKFTSADSVSYGIVMVEVMSYGERPYWMTNQDVINA 838
Db 778 TVTSALGOKIPIRWTAPPAIQAIRKFTSADSVSYGIVMVEVMSYGERPYWMTNQDVINA 837
QY 839 ISODYRLPPMPCPSALHOLMDCWQDRNRPFGQIVNTLDKMRPNPSIKAMAPLSS 898
Db 838 IEQDYRLPPMPCPSALHOLMDCWQDRNRPFLAEIVNTLRPMIRNPASLKTATIPA 897
QY 899 GINLLDORTPYDTSFNVTDEWLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGV 958
Db 898 VPSQPLDRLSIPDISAFTSVDLWLSAIKMGQYRDNFLSSGFTSLQVLAQMTSEDLLRIGI 957
QY 959 TLAGHOKILINSIQWRAQMNQ 980
Db 958 TLAGHOKILINSIQSMRVQITQ 979

RESULT 5
150612
protein-tyrosine kinase (EC 2.7.1.112) Cek6 - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Feb-2000
C:Accession: I50612; S33503
R:Sajjadi, F.G.; Pasquale, E.B.
Oncogene 8, 1807-1813, 1993
A:Title: Five novel avian Eph-related tyrosine kinases are differentially expressed.
A:Reference number: I50611; MUID:93288394; PMID:8510926
A:Accession: I50612
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-952 <SAJ>
A:Cross-references: EMBL:Z19110; NID:9312901; PIDN:CAA79526.1; PID:g312902
C:Gene: Cek6
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: Atp; phosphotransferase; transmembrane protein; tyrosine-specific protein kin
F:585-853/Domain: protein kinase homology <KIN>
F:593-601/Region: protein kinase ATP-binding motif
F:876-942/Domain: SAM homology <SAM>

Query Match 71.8%; Score 3724; DB 2; Length 952;
Best Local Similarity 70.3%; Pred. No. 5.9e-163;
Matches 688; Conservative 121; Mismatches 118; Indels 52; Gaps 3;

QY 21 ETLMDSSTATAELGWMVHPSPGSEVSGYDENMTIRYQVNCNVFESSONNMLRTKFIIR 80
Db 1 ETLMDSSTATAELGWMVHPSPGSEVSGYDENMTIRYQVNCNVFESSONNMLRTKFIIR 60
QY 81 RGAHRHVENKFSVRDCSSIPSPGSCKETFNLYYYEADFDPSATKTFPNNMENPVKVDIT 140
Db 61 RGAHRHVENKFSVRDCSSIPSPGSCKETFNLYYYEADFDPSATKTFPNNMENPVKVDIT 120
QY 141 IAADESFQVDLGGRWKINTEVRSFGVSRSGFLAPQDYGCGMSLIAVRVYFKCPRI 200
Db 121 IAADESFQVDLGGRWKINTEVRSFGVSRSGFLAPQDYGCGMSLIAVRVYFKCPRI 148
QY 201 IONGAIFQETLSGAESTSLVAARGSCITANAEEVDVPIKLYCNGDGEWLVPIGRCMKAGF 260
Db 149 VONFAIFPETMTGAESTSLVTARGTCIPNAEEVDVPIKLYCNGDGEWLVPIGRCMKAGF 208
QY 261 EAVENGTVCRGCPSGTFFKANQGDGDEACTHCPINSRTTSEGATNCVCRNGYRADLPLDMP 320
```



RESULT 7  
S37627  
protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: S37627  
R;Bohme, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Streibhardt, K.; Ruebe  
Oncogene 8, 2857-2862, 1993  
A;Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.  
A;Reference number: S37627; MUID:93390963; PMID:8397371  
A;Accession: S37627  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-998 <BO>  
A;Cross-references: UNIPROT:P54753; EMBL:X75208; NID:9406867; PIDN:CA53021.1; PID:g4068  
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat H  
C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki  
F;631-899/Domain: protein kinase homology <KIN>  
F;639-647/Region: protein kinase ATP-binding motif  
F;922-988/Domain: SAM homology <SAM>

Query Match 70.6%; Score 3661.5; DB 2; Length 998;  
Best Local Similarity 70.2%; Pred. No. 4.4e-160;  
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

Qy 10 LLLPL-----AAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCN 63  
Db 23 LLLPLLLPAGCRALBETLMDTKWVTSALWTSHPESGWEEVSGYDEANMPTIRTYQVCN 82

Qy 64 VFESSQNNMLRTKFIIRRGAAHRIHVENKFSVRDCSSIPSPGSKETFNLYYEADPDSA 123  
Db 83 VRESSQNNMLRTGFIWRDQVRYVVELKFTVRDCNSIPNIPGSKETFNLYYEADSDVA 142

Qy 124 TKTFNNMENPWKVDITIADESQVDLGRVWKINTEVRSFGPVSRSGFYLAFOYGG 183  
Db 143 SASPFWMENPYKVDITIADESFSRLDAG----RVNTKVRSGPLSKAGFYLAFOQGA 198

Qy 184 CMSLIARVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 243  
Db 199 CMSLIARVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 258

Qy 244 DGEWLVPGRGCMKAGFEAVENGTVCRGCPSTGTFKANKQGDCACTHCPINSRTTSEGATNC 303  
Db 259 DGEWVPVGACTCATGHEPAKESQCRPPGSKYKAKQGEPCPLPCPPNSRTTSPAASIC 318

Qy 304 VCRNGYRADLPDLMPCCTTIPSAQAVISSVNETSLMLEWTPPRDSGGEDLVYNIICK 363  
Db 319 TCHNNFYRADSDSADACTTVPSPRGVSNVNETSLILEWSEPRDLGVRDILLYNNVICK 378

Qy 364 SC--GSGRGACTRCGDNVQAPROGLTEPRIVISDILAHTQYTFEIQAVNGVTDQSPFS 421  
Db 379 KCHGAGASACRDCDDNVFVPRQLGSEPRVHTSHLLAHTRYTFEIQAVNGVSGKSLP 438

Qy 422 PQFASVNTTQAAAPSASVIMHQVSRVDSITLSWSQDQPNQVILDYELQYKELSEY 481  
Db 439 PRYAANVTITQAAPESEVPTLRHSSSGSLTSLWAPERPNGVILDYENKYEK--SEG 496

Qy 482 NATAKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGMVPQTMTE-AYEQTSLOEK 540  
Db 497 IASTVTSQMSVQDGLRPARYVQVARTVAGYGRYSGMVPQTMTE-AYEQTSLOEK 556

Qy 541 LPLIGSSAAGFLIAVWVIAVCNRRGFRADSEYDKLOHYTSGHMTPGMKIYIDPF 600  
Db 557 LPLVGSATAGLVFVAVVIAVCLRKQRHGSSEYTEKLOQY----IAPGMKVIYIDPF 612

Qy 601 TYEDPNAVREFAXEIDISCVKIEQVITGAGFVGVCSGHLKLPKRIEIVAIKTLKGYT 660  
Db 613 TYEDPNAVREFAXEIDVSCVKEBEVIGAGFVGVCSGHLKLPKRIEIVAIKTLKGYT 672

Qy 661 EKQRDFLSEASIMGQFDHPNVIHLEGVWTKSTFVMLITFERMENGSLDSFLRQNDQGVTV 720  
Db 661 EKQRDFLSEASIMGQFDHPNVIHLEGVWTKSTFVMLITFERMENGSLDSFLRQNDQGVTV 720

Db 673 ERQRDFLSEASIMGQFDHPNVIHLEGVWTKSTFVMLITFERMENGSLDSFLRQNDQGVTV 732

Qy 721 IQLVGMRLGIAAGMKYLADNMYVHRDLAARNILVNSNLVCKVSDFGSLFLEDDTSDPTTY 780  
Db 733 IQLVGMRLGIAAGMKYLSENNYVHRDLAARNILVNSNLVCKVSDFGSLFLEDDTSDPTTY 792

Qy 781 TSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIVMVMSYGERPYDMTQDVINAIE 840  
Db 793 TSSLGKIPIRWTAPEAIYRKFTSASDVMSYGIVMVMSYGERPYDMTQDVINAIE 852

Qy 841 QYRLPPMDCPSALHQLMDCWQDRNHRPFQGIWTLDKMIRNPNSLKAMAPLSSGI 900  
Db 853 QYRLPPMDCPTALHQLMDCWVRDRNLRPFQSIWTLDKLIRNAASLKVIASAQSG 912

Qy 901 NLPLDRTTIPDYTFNTVDWLEAIKMGQYKESFANAGTFSFDVVSQMMMEDILRLGVTL 960  
Db 913 SQPLDRTTIPDYTFNTVDWLEAIKMGQYKESFANAGTFSFDVVSQMMMEDILRLGVTL 972

Qy 961 AGHQKILNSIQVMRAQMNQIQSVEV 986  
Db 973 AGHQKILNSIQVMRAQMNQIQSVEV 998

RESULT 8  
I48653  
mouse developmental kinase 5 (MDK5) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48653  
R;Clossek, T.; Lerch, M.M.; Ullrich, A.  
Oncogene 11, 2085-2095, 1995  
A;Title: Cloning, characterization, and differential expression of MDK2 and MDK5, two no  
A;Reference number: I48652; MUID:96074837; PMID:7478528  
A;Accession: I48653  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-993 <RES>  
A;Cross-references: UNIPROT:P54754; EMBL:Z49086; NID:g108989; PIDN:CA88910.1; PID:g1089  
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat H  
C;Keywords: ATP; transmembrane protein  
F;626-894/Domain: protein kinase homology <KIN>  
F;634-642/Region: protein kinase ATP-binding motif  
F;917-983/Domain: SAM homology <SAM>

Query Match 70.0%; Score 3630.5; DB 2; Length 993;  
Best Local Similarity 69.8%; Pred. No. 1.1e-158;  
Matches 690; Conservative 113; Mismatches 165; Indels 21; Gaps 6;

Qy 9 ALLLLPILA-----AVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCN 63  
Db 15 APLLPLLLPAGCWALEETLMDTKWVTSALWTSHPESGWEEVSGYDEANMPTIRTYQVCN 74

Qy 64 VFESSQNNMLRTKFIIRRGAAHRIHVENKFSVRDCSSIPSPGSKETFNLYYEADPDSA 123  
Db 75 VRESSQNNMLRTGFIWRDQVRYVVELKFTVRDCNSIPNIPGSKETFNLYYEADSDVA 134

Qy 124 TKTFNNMENPWKVDITIADESQVDLGRVWKINTEVRSFGPVSRSGFYLAFOYGG 183  
Db 135 SASPFWMENPYKVDITIADESFSRLDAG----RVNTKVRSGPLSKAGFYLAFOQGA 190

Qy 184 CMSLIARVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 243  
Db 191 CMSLIARVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 250

Qy 244 DGEWLVPGRGCMKAGFEAVENGTVCRGCPSTGTFKANKQGDCACTHCPINSRTTSEGATNC 303  
Db 251 DGEWVPVGACTCATGHEPAKESQCRPPGSKYKAKQGEPCPLPCPPNSRTTSPAASIC 310

Qy 304 VCRNGYRADLPDLMPCCTTIPSAQAVISSVNETSLMLEWTPPRDSGGEDLVYNIICK 363  
Db 311 TCHNNFYRADSDSADACTTVPSPRGVSNVNETSLILEWSEPRDLGVRDILLYNNVICK 370

Qy 364 SCGSGRGA----CTRCGDNVQAPROGLTEPRIVISDILAHTQYTFEIQAVNGVTDQGS 418  
Db 364 SCGSGRGA----CTRCGDNVQAPROGLTEPRIVISDILAHTQYTFEIQAVNGVTDQGS 418



```
Db 371 KCRSSGAGGATCSRCDNNVEFVRQLGLTERVHSHLLAHRTYTFEVAQVNGVSGKS 430
Qy 419 PFSQFASVNTTNOAAPSAVSIHQVSRVSDITLWSQDQDPNGVILDYELQYKEKL 478
Db 431 PLPRYAANVTNOAAPSEVPTLHSHSSGSLTSLWAPERNGVILDYEMKYFEK-- 488
Qy 479 SEYNATAIKSPNTVTVOGLKAGAIYVQVRAARTVAGRYSGKQYFOTWTE-AEYQTSI 537
Db 489 SKGIASVTSSOKNSVQLDGLQPDARYVQVRAARTVAGRYSGKQYFOTWTE-AEYQTSI 548
Qy 538 QEKLPLIIGSSAAGLVFLIAVVTIAVNCNRGFERADSEYTDKLOHTYSGHMTGKMIYI 597
Db 549 QEQLPLVIGSVAGVFMVMMVVIALVCLRKQRHGPDAEYTEKLOQY----IAPGMKVYI 604
Qy 598 DPFTYEDPNEAVREFAKEIDISCVKIEBIVGAGFGEVCSGHLKPGKREIFVAIKTLKS 657
Db 605 DPFTYEDPNEAVREFAKEIDISCVKIEBIVGAGFGEVCSGHLKPGKREIFVAIKTLKV 664
Qy 658 GYTEKQRDFLSEASINGQDPHPNVHLEGVVTKSTPVMITFPMENGLSDSFLRQNDGQ 717
Db 665 GYTEKQRDFLSEASINGQDPHPNIIRLEGVVTKSRPVMILTEPMENCALDSFLRLNDGQ 724
Qy 718 FTVLQVGLRGIAAGMKYLADNMVYHVDLAARNILVNSNLVCKVSDFGLSRPLEDDTSD 777
Db 725 FTVLQVGLRGIAAGMKYLSEMYVHVDLAARNILVNSNLVCKVSDFGLSRPLEDDTSD 784
Qy 778 PTTYSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMNQDVIN 837
Db 785 PTTYSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMNQDVIN 844
Qy 838 AIEQDYRLPPMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLS 897
Db 845 AVEQDYRLPPMDCPTALHQLMDCWDRNLRNPKFSQIVNTLDMIRNPNLSKAMAPLS 904
Qy 898 SGINPLDRTIPDYTSFNTVDEWLEAKQYKESFANAGFTSFVDVMSQMMEDIIRLG 957
Db 905 SGMSQPLDRTVPDYTTFTTVDWLDIAKQYKESFVAGFASFDLVAQWTAEDLLRIG 964
Qy 958 VTLAGHOKKILNSIQVNRANQIQSVSEV 986
Db 965 VTLAGHOKKILCSIQDMRLQNNQTLPVQV 993

RESULT 9
I49071
protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed in the myocardium of the deve
A;Reference number: I49071; MUID:95200796; PMID:7893599
A;Accession: I49071
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-938 <RES>
A;Cross-references: UNIPROT:Q60669; EMBL:U11493; NID:G595418; PIDN:AAA67925.1; PID:G5954
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
F;571-839/Domain: protein kinase homology <KIN>
F;579-587/Region: protein kinase ATP-binding motif
P;862-928/Domain: SAM homology <SAM>

Query Match 66.3%; Score 3441; DB 2; Length 938;
Best Local Similarity 68.9%; Pred. No. 4.9e-150;
Matches 653; Conservative 113; Mismatches 166; Indels 16; Gaps 6;

Qy 45 EVSGVDENMTIRYQVNCNPVSESSONWLRKTFIRRRGAHRIHYEMKFSVRDCSSIPSVP 104
Db 1 EVSGDEAMNPIRTYQVNCNPVSESSONWLRKTFIRRRGAHRIHYEMKFSVRDCSSIPSVP 60
```

```
Qy 105 GSKCTFNLYYYEADFDSDATKTFPNMNMENPMWVKVDITTAADSESPQVLDGGRVWKINTEVR 164
Db 61 GSKCTFNLYYYEADSDVASASSPFWNMENPMWVKVDITTSDESFSR-SMPGRV---NTRKV 116
Qy 165 SFGPVSRSGLVAFODYGGCWSLIAVRFVYKCPRI11QNGAIFOETLSGAESTSLVAARG 224
Db 117 SFGPLSKAGYGLGFDQOQACMSLISVRAFVYKCASTTAGTALFPETITUGAETSLV1APR 176
Qy 225 SCIANABEVDPVILKLCNGDGEWLPIGRCMCKAGFEAVENGTVCRCGPCSGTFFKANQODE 284
Db 177 ACIANAVEVSVPLKLCNGDGEWMVPGVACTCATGHEPAAKESQCRACPPGSKAKQGE 236
Qy 285 ACTHCPINSTTSEGATNCVRNGYTRADLDLPMPCTTTPSAQOAVISSVNETSLMLEW 344
Db 237 PCLPCPNSTRTTSPAASICTCHNFVRADSDSADTCTRRSPRGVINSVNETSLLEW 296
Qy 345 TPRDSDGREDLVNIIICKSGSGRGA-----CTRCGDNVOYAPRQLGLTEPRYIISDLL 399
Db 297 SEPRDLGGRDLDLVNICKCRGSSGAGGATCSRCDNNVEFVRQLGLTERVHSHLL 356
Qy 400 AHTQYTFEIOAVNGVTDQSPFSQFASVNTTNOAAPSAVSIHQVSRVSDITLWSQ 459
Db 357 AHTRYTFEIOAVNGVSGSKSPLPRYAANVTNOAAPSEVPTLHSHSTSGSLTSLWAP 416
Qy 460 DQNGVILDYELQYKEKSEYNATAIKSPNTVTVOGLKAGAIYVQVRAARTVAGRY 519
Db 417 ERPNGLVDYEMKYFEK--SKAIASVTSSOKNSVQLDGLQPDARYVQVRAARTVAGRY 474
Qy 520 SGRMYFOTWTE-AEYQTSIOEKLPLIIGSSAAGLVFLIAVVTIAVNCNRGFERADSEY 578
Db 475 THPAEFETTSERGSAQQLQEQPLVIGSVNAGVFMVMMVVIALVCLRKQRHGPDAEY 534
Qy 579 DKLOHTYSGHMTGKMIYIDPFTYEDPNEAVREFAKEIDISCVKIEBIVGAGFGEVCSG 638
Db 535 EKLOQY----IAPGMKVYIDPFTYEDPNEAVREFAKEIDISCVKIEBIVGAGFGEVCSG 590
Qy 639 HLKLPGRKREIFVAIKTLKSGYTEKQRDFLSEASINGQDPHPNVHLEGVVTKSTPVMII 698
Db 591 RLKLPGRREVFVAIKTLKVGYTEKQRDFLSEASINGQDPHPNIIRLEGVVTKSRPVMIL 650
Qy 699 TEFMENGSLDSFLRQNDGQFTVLQVGLRGIAAGMKYLADNMVYHVDLAARNILVNSNL 758
Db 651 TEFMENCALDSFLRLNDGQFTVLQVGLRGIAAGMKYLSEMYVHVDLAARNILVNSNL 710
Qy 759 VCKVSDFGLSRPLEDDTSDPTYSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMVE 818
Db 711 VCKVSDFGLSRPLEDDTSDPTYSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMVE 770
Qy 819 VMSYGERPYWDMNQDVINAIEQDYRLPPMDCPSALHQLMDCWQKDRNHRPKFGQIVN 878
Db 771 VMSYGEQPYWNMSNQDDINAVEQDYRLPPMDCPTALHQLMASCWVRDRNLRPKFSQIVN 830
Qy 879 TLDKMTIRNPNLSKAMAPLSGINPLDRTIPDYTSFNTVDEWLEAKQYKESFANAG 938
Db 831 TLDKLRNPNLSKAMAPLSGINPLDRTVPDYTTFTTVDWLDIAKQYKESFVAG 890
Qy 939 FTSFDDVVSQMMEDIIRLGVTLAGHOKKILNSIQVNRANQIQSVSEV 986
Db 891 FASFDLVAQWTAEDLLRIGVTLGHHQKILCSIQDMRLQNNQTLPVQV 938

RESULT 10
I51549
receptor tyrosine kinase - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
R;Winning, R.S.; Sargent, T.D.
Mech. Dev. 46, 219-229, 1994
A;Title: Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has 1
A;Reference number: I51549; MUID:95001564; PMID:7918105
A;Accession: I51549
A;Status: preliminary; translated from GB/EMBL/DBJ
```



Db 553 VSVTVGVILLAVIGVLLSGRRCCYSKAKQDPBEEKMHFNHGHKLPVGRVYIDPHTYED 612  
Qy 605 PNEAVRFAKEIDISCVKIEQVIGAGFEGVCSGHLKLPGRKRFVFAIKTLKSGYTEKOR 664  
Db 613 PNOAVHEFAKEIEASCITIBRVIGAGFEGVCSGRLKLPGRRLPVAIKTLKGYTEKOR 672  
Qy 665 RDLSEASIMQGDHPNVIHLEGVVTKSTPMIITEFMENGSLDSFLRQNDGQFTVIQLV 724  
Db 673 RDLFGEASIMQGDHPNVIHLEGVVTKSTPMIITEFMENGSLDSFLRQNDGQFTVIQLV 732  
Qy 725 GMLRGIAAGKYLADMMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYSAL 784  
Db 733 GMLRGISAGKYLSDMGVYHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYSAL 790  
Qy 785 GGIPIRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQDVINAIEQDYR 844  
Db 791 GGIPIRTWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQDVINAIEQDYR 850  
Qy 845 LPPPMDCPSALHQLMLDCWQKRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPL 904  
Db 851 LPPPMDCPSALHQLMLDCWQKRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPL 910  
Qy 905 LDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVSVQMMEDILRLGVTLAGHQ 964  
Db 911 AEHSPLGSGAYRSYGVLEAIKMGRYTEIFEMGYSSMDAVAQVTLDRRLGLVTLVGHQ 970  
Qy 965 KKIILNSIQVMRAQM 978  
Db 971 KKIILNSIQVMRAQM 984

RESULT 12  
178844  
receptor protein-tyrosine kinase - human  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I78844  
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janseen, A.M.; Basu, R.; Welcher,  
Oncogene 10, 897-905, 1995  
A;Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty  
A;Reference number: I58351; MUID:95206782; PMID:7898931  
A;Accession: I78844  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-986 <RES>  
A;Cross-references: UNIPROT:P54764; GB:L36645; NID:G551613; PIDN:AAA74246.1; PID:G551614

Query Match 58.7%; Score 3045; DB 2; Length 986;  
Best Local Similarity 59.3%; Pred. No. 6.3e-132;  
Matches 580; Conservative 146; Mismatches 112; Indels 40; Gaps 12;  
Qy 18 AVETLMDSTATATAEIGMWHVP-PSGWEVSGVDENMNTIRTVQVNCVFNSSQNNMLRTK 76  
Db 28 ANEVTLDSRSVOGELGWIASPLEGGWEVSIIMDEKNTPIRTVQVNCVFNSSQNNMLRTD 87  
Qy 77 FIRRRAHRIHVEMKFGVRDCSSIPSPVSGCKETFNLYYYEADPDSATKTFPNWMEHPV 136  
Db 88 WITTEGAQRVYIEKFTLRDCNSLPVGMGTCKETFNLYYYESDNDKERFI----RENQFV 143  
Qy 137 KVDTIADESFQVDLGGRVNWKINTEVRSGFVSRSGFYLAPODYGCMSLIARVVPYRK 196  
Db 144 KIDTIADESFTQVDIGDRIMKLNTEIRDVGPLSKGFLAFQDVGACIALVSVRVYFKK 203  
Qy 197 CPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVVDVPIKLYCNGDGEWLPVIGCMC 256  
Db 204 CPLTVRNLAQFPDPTITGADTSSSLVEVRGSCVNNSEKQVFP-RMYCGADGEWLPVIGNCLC 262

Qy 257 KAGFEAVENGTVCRGCPSGTFRKANQDEACTHCPINSRITTSAGTNCVCRNGYYRADLDP 316  
Db 263 NACHE--ERSGEQACKIGYVKALSTDATCAKCPHPSYSVMEGATSCCTDGRGFFRADNDA 320  
Qy 317 LDMPCITTIAPQAVISSLVNETSLMLEWTPPRDSGGREDLVNLI CKSCSG- RGACTRC 375  
Db 321 ASMPCTRPSPAPLNLISNVNETSVNLEWSPQNTGGRQDISYNVWCKKCGAGPSPKCRPC 380  
Qy 376 GDNVQAPRQLGTEPRIYISDILLAHTQYTFEIQAVNGVTDQSPFPSPQFASVNIITNQAA 435  
Db 381 GSGVHTYTPQNGLKTKTKVSTIDLLAHTNYTFELWANGVSKYNPNPDQSVVTVTNQAA 440  
Qy 436 PSASIMHQVSRVDSITLSWSDQDPNGVILDYELQYKEKSEYNATAIKSPTNTVT 495  
Db 441 PSSIALVQAEKVTYRSVALAWLEPDRPNGVILEYEVKYEKQDNERSYRIVTAARNTDI 500  
Qy 496 QGLKAGAIYVQVRAARTVAGYGRYSKMYFQTMTEAEYQTSIQEKLPL-LIIGS----- 547  
Db 501 KGLNPLTYSYVHRARTAAAGYDGSFPLEVTNT-----VPSRIIGCANSTVL 549  
Qy 548 --SAAGLVFLIAVWIAIVCNRR--GFERADSEYTDKLQHYTSGHMTPGMKIYIDPPTYE 603  
Db 550 LVSVSQSVLVVLLIAAFVISRRSKYKAKQADEE-----KHLNQGVRTYVDPTYE 603  
Qy 604 DPNEAVREFAKEIDISCVKIEQVIGAGFEGVCSGHLKLPGRKRFVFAIKTLKSGYTEKQ 663  
Db 604 DPNEAVREFAKEIDISCVKIEQVIGAGFEGVCSGHLKLPGRKRFVFAIKTLKAGYTDKQ 663  
Qy 664 RRDFLSEASIMQGDHPNVIHLEGVVTKSTPMIITEFMENGSLDSFLRQNDGQFTVIQL 723  
Db 664 RRDFLSEASIMQGDHPNVIHLEGVVTKSTPMIITEFMENGSLDSFLRQNDGQFTVIQL 723  
Qy 724 VGMRLGIAAGKYLADMMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYSAL 783  
Db 724 VGMRLGISAGKYLSDMGVYHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYSAL 782  
Qy 784 LGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQDVINAIEQDY 843  
Db 783 -GGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMNQDVINAIEQDY 841  
Qy 844 RLPPPMDCPSALHQLMLDCWQKRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLP 903  
Db 842 RLPPPMDCPSALHQLMLDCWQKRNHRPKFGQIVNTLDMIRNPNLSKRTGTSSSRNTA 901  
Qy 904 LDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVSVQMMEDILRLGVTLAGH 963  
Db 902 LLDPSPEPESAVSVSGDWLQAIKMDRYKDNFTAGVTILEAVVHVNQEDLARIGITATH 961  
Qy 964 QKKILNSIQVMRAQMNOI 981  
Db 962 QNKILSSVQAMRTQMOM 979

RESULT 13  
S78059  
protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: S78059; S30505; I58366  
R;Charnay, P.  
submitted to the EMBL Data Library, March 1992  
A;Reference number: S78059  
A;Accession: S78059  
A;Molecule type: mRNA  
A;Residues: 1-986 <CHA>  
A;Cross-references: UNIPROT:Q03137; EMBL:X65138; NID:G54083; PIDN:CAA46268.1; PID:G54084  
R;Gillardi-Habenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chestier, A.; Wilkinson,  
Oncogene 7, 2499-2506, 1992  
A;Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in t  
A;Reference number: S30496; MUID:93096484; PMID:1281307  
A;Accession: S30505  
A;Molecule type: mRNA  
A;Residues: 1-31,55-986 <GIL>



Db 503 NNLKPGTVYVQIRAFATAGYNTSPRLDVALEATGKMFPAVASEQNPFVIIIAVVA 562  
Qy 549 AAGLVFLIAVVAIAVCNRR-GPERADSEYTDKLOHYTSGHMTGMIYIDPFTYEDPNE 607  
Db 563 VAGTIIILVFWVFGIIGRRHCGYSKADQEGDEELYFH---FKPGTKTYIDPETYEDPNR 619  
Qy 608 AVREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDF 667  
Db 620 AVHQFAKELDASCIKIERVIGAGFGEVCSGRLKLPGRDVAVAIKTLKVGYTEKQRDF 679  
Qy 668 LSEASINGQDHPNVHLEGVVTKSTPMIITEFMWNGSLDSFLRQNDGQFTVQLVGML 727  
Db 680 LCEASINGQDHPNVHLEGVVTKSTPMIITEFMWNGSLDSFLRQNDGQFTVQLVGML 739  
Qy 728 RGIAAGKYLADNMVYHVRDLAARNILNSNLVCKVSDFGLSRFLEDDTSDPTYSALGGK 787  
Db 740 RGIAAGKYLADNMVYHVRDLAARNILNSNLVCKVSDFGLSRFLEDDTSDPTYSALGGK 797  
Qy 788 IPIRWTAPETAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNDQVINAIEQDYRLPP 847  
Db 798 IPIRWTAPETAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNDQVINAIEQDYRLPP 857  
Qy 848 PMDCPSALHQLMDCWQKRAERPKFQIIVNTLDKMIARNPNSLKAMAPLSGGINLPDDR 907  
Db 858 PMDCPSALHQLMDCWQKRAERPKFQIIVNTLDKMIARNPNSLKAMAPLSGGINLPDDR 917  
Qy 908 TIPDYTEFNTVDEWLEAIKMGQYKESFANAGFTSDFVVSOMMEDILRLGVTLVGHOKKI 967  
Db 918 NTPDFTFCVSGEVLQAIKMYRYKDNFTAAAGNSLESVARMTIEDVMSGLGTLVGHOKKI 977  
Qy 968 LNSIQVNRQAM 978  
Db 978 MSSIIQTMRQAM 988

RESULT 15  
JC5672  
receptor tyrosine kinase (EC 2.7.-.-) EbK precursor - mouse  
N;Alternate names: developmental kinase 1  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Nov-1997 #sequence\_revision 20-Nov-1997 #text\_change 09-Jul-2004  
C;Accession: JC5672; I48611; S51740  
R;Talukder, A.H.; Muramatsu, T.; Kaneda, N.  
Cell Struct. Funct. 22, 477-485, 1997  
A;Title: A novel truncated variant form of EbK/MDKI receptor tyrosine kinase is expressed  
A;Reference number: JC5672; MUID:98035156; PMID:9368721  
A;Accession: JC5672  
A;Molecule type: mRNA  
A;Residues: 1-998 <TAL>  
A;Cross-references: UNIPROT:Q61772  
A;Experimental source: embryo  
R;Closek, T.; Millaer, B.; Ullrich, A.  
Oncogene 9, 97-108, 1995  
A;Title: Identification of alternatively spliced mRNA encoding variants of MDKI, a novel  
A;Reference number: I48611  
A;Accession: I48611  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-998 <RES>  
A;Cross-references: EMBL:X79082; NID:9607133; PID:CAA55687.1; PID:9607134  
C;Comment: This enzyme plays a role during development involving differentiation and pro  
C;Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat h  
C;Keywords: ATP; brain; phosphotransferase; transmembrane protein  
P;1-30/Domain: signal sequence #status predicted <SIG>  
P;31-998/Product: receptor tyrosine kinase EbK #status predicted <MAT>  
P;31-553/Domain: extracellular #status predicted <EXT>  
P;331-438/Domain: fibronectin type III repeat <FN1>  
P;441-534/Domain: fibronectin type III repeat <FN2>  
P;554-579/Domain: transmembrane #status predicted <TM>  
P;631-897/Domain: protein kinase homology <KIN>  
P;639-847/Region: protein kinase ATP-binding motif  
P;920-986/Domain: SAM homology <SAM>

Query Match 58.1%; Score 3013; DB 2; Length 998;  
Best Local Similarity 58.6%; Pred. No. 1.8e-130;  
Matches 572; Conservative 157; Mismatches 217; Indels 30; Gaps 11;  
Qy 17 AAVEETLMDSTTAAELGVMVHPSPGWEVSGVDENMTTIRTYQVNCVFSSQNNWLRTK 76  
Db 29 AAKEVLDDSKAQTTELEWISSPPSGWEEISGLDENYTPIRTYQVNCVFSSQNNWLRTN 88  
Qy 77 FIRRGAHRTHVMKFSVRDCSSIPSPVPGCKETFNLYYEADPDSATKTPPNMNPWV 136  
Db 89 WISKGNARLFLVKLFLTRDCNSLPGVLGCKETFNLYYEADPDSATKTPPNMNPWV 144  
Qy 137 KVTIIADEFSDVLDGGRVMKINTEVRSFGVSRSGFYLAFOYGGCMSLIAVRVYRK 196  
Db 145 KIDTIAADESFTQDLGERKMKLNTREVGIPGLSKGYLAFOYGGCMSLIAVRVYRK 204  
Qy 197 CPRIIONGALFOETLSGAESTSLVAARGCIANA-BEVDVPIKLYCNGDGEWLVPIGRM 255  
Db 205 CWTIVENLAVFPDVTGSEFSLVEVRGTCVSSAAESEAENSPRMHCSAEGEWLVPIGKI 264  
Qy 256 CKAGFEAVENGTVCRGCPGSGTFRANQGDCACTHCPIINSRTTSEGATNCVCRNGYRADLD 315  
Db 265 CKAGIQ--QKGDTCPCGRRFYKSSSQDLQSCRPTHFSFDRGSSRCBCEGYRAPSD 322  
Qy 316 PLDMPCPTTIPSAQVATISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTRC 375  
Db 323 PPVACTRPPSAQNLFINQITVSLWSPADNGGRNDVTVRIILCKRCSWEQEGCVPC 382  
Qy 376 GDNVQAPROGLTEPRIYISDLAHTQYTFEQAQVNGVTDQSPFPQFASVNTTQAA 435  
Db 383 GSNIGYMPQOTGLEDNVTVMDLAAHANYTFEVAENVGSDLSRSQRLFAAVSITGQAA 442  
Qy 436 PSASVIMHOVSRTVDSITLWSOPDQNGVILDVLOYEYKELSEYNATAIKSPNTTVV 495  
Db 443 PSQVGVMKERVLORSVQLSNQEPHENGVTETIYKYEKQERERTYSLTKSTAS 502  
Qy 496 QGLKAGAIYVQVARTVAGYGRYSGMYFQMTTEA-----EYQTSIQEKLPLIGS--S 548  
Db 503 NNLKPGTVYVQIRAFATAGYNTSPRLDVALEASGKMFPAVASEQNPFVIIIAVVA 562  
Qy 549 AAGLVFLIAVVAIAVCNRR-GPERADSEYTDKLOHYTSGHMTGMIYIDPFTYEDPNE 607  
Db 563 VAGTIIILVFWVFGIIGRRHCGYSKADQEGDEELYFH---FKPGTKTYIDPETYEDPNR 619  
Qy 608 AVREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDF 667  
Db 620 AVHQFAKELDASCIKIERVIGAGFGEVCSGRLKLPGRDVAVAIKTLKVGYTEKQRDF 679  
Qy 668 LSEASINGQDHPNVHLEGVVTKSTPMIITEFMWNGSLDSFLRQNDGQFTVQLVGML 727  
Db 680 LCEASINGQDHPNVHLEGVVTKSTPMIITEFMWNGSLDSFLRQNDGQFTVQLVGML 739  
Qy 728 RGIAAGKYLADNMVYHVRDLAARNILNSNLVCKVSDFGLSRFLEDDTSDPTYSALGGK 787  
Db 740 RGIAAGKYLADNMVYHVRDLAARNILNSNLVCKVSDFGLSRFLEDDTSDPTYSALGGK 797  
Qy 788 IPIRWTAPETAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNDQVINAIEQDYRLPP 847  
Db 798 IPIRWTAPETAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNDQVINAIEQDYRLPP 857  
Qy 848 PMDCPSALHQLMDCWQKRAERPKFQIIVNTLDKMIARNPNSLKAMAPLSGGINLPDDR 902  
Db 858 PMDCPSALHQLMDCWQKRAERPKFQIIVNTLDKMIARNPNSLKAMAPLSGGINLPDDR 912  
Qy 903 PLIDRTIPDYSNTVDEWLEAIKMGQYKESFANAGFTSDFVVSOMMEDILRLGVTLVGH 962  
Db 913 PLIDQSTPDFTAFCSGVEVLQAIKMYRYKDNFTAAAGNSLESVARMTIEDVMSGLGTLV 972  
Qy 963 HOKKILNSIQVNRQAM 978  
Db 973 HOKKIMSSIIQTMRQAM 988

RESULT 16

I50615

receptor-type protein-tyrosine kinase Cek7, long splice form - chicken

C;Species: Gallus gallus (chicken)

C;Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text\_change 09-Jul-2004

C;Accession: I50615; I50616; I50614

R;Siever, D.A.; Verderame, M.F.

Gene 146, 219-226, 1994

A;Title: Identification of a complete Cek7 receptor protein tyrosine kinase coding sequence

A;Reference number: I50614; MUID:95047429; PMID:7958948

A;Accession: I50615

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1013 <SIE>

A;Cross-references: UNIPROT:P54755; EMBL:U03910; NID:9555617; PID:AAB60612.1; PID:95556

A;Accession: I50616

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-572, 'R', 596-1013 <S12>

A;Cross-references: EMBL:U03910; NID:9555617; PID:AAB60613.1; PID:9555619

A;Accession: I50614

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-279, 444-572, 'R', 596-1013 <S13>

A;Cross-references: EMBL:U03910; NID:9555617; PID:AAB60614.1; PID:9555620

C;Genetics:

A;Gene: Cek7

C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

C;Keywords: alternative splicing; ATP; transmembrane protein

F;649-915/Domain: protein kinase homology <KIN>

F;657-665/Region: protein kinase ATP-binding motif

F;938-1004/Domain: SAM homology <SAM>

Query Match 58.0%; Score 3009; DB 2; Length 1013;

Best Local Similarity 57.0%; Pred. No. 2.8e-130;

Matches 568; Conservative 165; Mismatches 229; Indels 34; Gaps 10;

QY 6 LGALLLLPLLAAYEETLMDSTTATAEALGVMVHPPSGWEEVSGYDENMTIRTYQVCNVF 65

DB 22 LCAALLRSLGSGEENLLDSRTVGLGWLAFKNGWEEIGEDVENVAPHTYQVCNVK 81

QY 66 ESSQNNWLRTKPIRRRGAHRIHVMKFSVPDCSSIPSGCKETFNLYYEADFDSATK 125

DB 82 EQQNNLLTSWISNEGSPASSFELKFTLRDCNSLPGGLGCKETFNMYFESDDEGR- 140

QY 126 TFPNMENPMVKVDITIADESPQVDLGRVWKNTEVRSFGVSRSGFYLAFOYDGC 185

DB 141 ---NIRENQYIKIDTIAADESFTELDLGRVWKNTEVRSFGVSRSGFYLAFOYDGC 197

QY 186 SLIAVRVFKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDG 245

DB 198 ALVSRVRYKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDG 256

QY 246 EWLVPTRGCMKAGFEAVENGTVRCGSPGTFKANOQDEACTHCIPINRTTSEGATNCVC 305

DB 257 EWLVPTRGCMKAGFEAVENGTVRCGSPGTFKANOQDEACTHCIPINRTTSEGATNCVC 314

QY 306 RNYGYRADLPLDPMCTTIPSAQAVISSVNETSLMLEWTPRDSGGREDLVNIIICKSC 365

DB 315 BEHYFRRESDDPTMACTRPSPAPRSAINSVNETSLMLEWTPRDSGGREDLVNIIICKSC 374

QY 366 GSGRGACTCGNVQVAPQLGLTEPRIYISLLAHTOYTFEIOAVNGVTQSPSPQFA 425

DB 375 NHHSGLCEACGSHVRLPQOTGLKNTSVNMVLLAHTNYTFEIAVNGVSDQNPQARQV 434

QY 426 SVNITNQAAAPSVMHGVSRVDSITLSWQPOPNVILDLLOYEYKELSEYNATA 485

DB 435 SVNITNQAAAPSVMHGVSRVDSITLSWQPOPNVILDLLOYEYKELSEYNATA 493

QY 486 IKSPTNTVTVGLKAGAIYVQVARTVAGYSGYSGMYFQNTWAEYQTSIQEKLPLII 545

DB 494 IKSPTNTVTVGLKAGAIYVQVARTVAGYSGYSGMYFQNTWAEYQTSIQEKLPLII 552

QY 546 GSSAAGLVFLIAVVVIAI---VCN-----RRGFERADSEYTDKLOH 583

DB 553 VSVTVGVILLAVVIFGLSGSCDHCWGASSLRAVAVPSLIMRCGYSKAQDPDEEKOH 612

QY 584 YTSGHM-TPGMKIYIDPPTYEDPNVAREFAKEIDISCVKIEQVIGAGEFVCSGHLKL 642

DB 613 FHNGHILKLPGRVYIDPPTYEDPNVAREFAKEIDISCVKIEQVIGAGEFVCSGHLKL 672

QY 643 PKRELFVAIKTLKSGYTEKORRDFLSASIMQGFDPHNVHLEGVVTKSTPVMIIITFM 702

DB 673 QKREFFVAIKTLKSGYTEKORRDFLSASIMQGFDPHNVHLEGVVTKSTPVMIIITFM 732

QY 703 ENGSLDSFLRQNDGQFTVIQVLMGLGIAAGMKYLADNMVYVHRDLAARNILVNSNLVKV 762

DB 733 ENGSLDTFLKNDGQFTVIQVLMGLGIAAGMKYLADNMVYVHRDLAARNILVNSNLVKV 792

QY 763 SDFGLSRFLEDDTSDPTTYSALGGKIPRTWTAPEAIQVKEKFTSASDVMSYGIWMVEVMSY 822

DB 793 SDFGLSRFLEDD-PEAAVYTR-GGKIPRTWTAPEAIQVKEKFTSASDVMSYGIWMVEVMSY 850

QY 823 GERPYDMTNQDVINAIEDYRLPPMDPCPSALHQLMDCQKDRNHRPKFQOIVNTLDK 882

DB 851 GERPYDMTNQDVINAIEDYRLPPMDPCPSALHQLMDCQKDRNHRPKFQOIVNTLDK 910

QY 883 MIRNPNSLKAMAPLSGGINLPLDRTIPDYSFNTVDWLEAIKMGQYKESFANAGFTSF 942

DB 911 LIRNPSSLATLVNASSRVSNNLVEHSPVSGSAYRSVGEWLEAIKMGRYTEIFMENGYSNM 970

QY 943 DVVSQMMEDILRLGVTLAGHOKKILNSIQVNRQOM 978

DB 971 DSAQVTELDRLRLGVTLAGHOKKILNSIQVNRQOM 1006

RESULT 17

S51604

receptor-like tyrosine kinase Etk-1 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 29-May-1998

C;Accession: S51604

R;Maisonnier, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.

Oncogene 8, 3277-3288, 1993

A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam

A;Reference number: S49015; MUID:94067777; PMID:7504232

A;Accession: S51604

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-981 <NAI>

A;Cross-references: EMBL:S68029

A;Note: the authors translated the codon GAC for residue 170 as Glu

C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

C;Keywords: ATP; transmembrane protein

F;651-917/Domain: protein kinase homology <KIN>

F;659-667/Region: protein kinase ATP-binding motif

Query Match 56.6%; Score 2939; DB 2; Length 981;

Best Local Similarity 58.3%; Pred. No. 4.3e-127;

Matches 552; Conservative 161; Mismatches 220; Indels 14; Gaps 10;

QY 6 LGALLLLPLLAAYEETLMDSTTATAEALGVMVHPPSGWEEVSGYDENMTIRTYQVCNVF 65

DB 48 LCAALLRSLGSGEENLLDSRTVGLGWLAFKNGWEEIGEDVENVAPHTYQVCNVK 107

QY 66 ESSQNNWLRTKPIRRRGAHRIHVMKFSVPDCSSIPSGCKETFNLYYEADFDSATK 125

DB 108 EQQNNLLTSWISNEGSPASSFELKFTLRDCNSLPGGLGCKETFNMYFESDDEGR- 166

QY 126 TFPNMENPMVKVDITIAADESFQVDLGRVWKNTEVRSFGVSRSGFYLAFOYDGC 185

DB 167 ---NIKQYIKIDTIAADESFTELDLGRVWKNTEVRSFGVSRSGFYLAFOYDGC 223

QY 186 SLIAVRVFKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDG 245

Db 224 ALVSRVYKCKSVRHLAVPDTITGADSSQLLEVGSCV-NHSTVDDPPKMHCSAEG 282  
Qy 246 EWLVPICRMCKAGFAVENGTGRCGPGSTGFKANQGDDEACTHCPINSRTTSETGATNCVC 305  
Db 283 EWLVPICRMCKAGYEE-KNGT-CQVCRPGFFKASPHSQICSKCPHPSYTHEEASTSCVC 340  
Qy 306 RNGYRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPRDSGGREDLVNIIKSC 365  
Db 341 EKDYFRRESPPPTWACTRPPSPAPRNAISNVNETSVFLEWIPPADTGGGKDVSYILCKKC 400  
Qy 366 GSGRGACTRCGDNVQAPROLGLTEPRIYISDLAHTQYTFEIOAVNGVTDOSPFSPQA 425  
Db 401 NSHAGVCEBGGHRYLPQQIGLKNVSMADPLAHTNYTFEIAVANGVSDLSGTRQYV 460  
Qy 426 SVNITTTQAAPSASVIMHQSRTVDSITLSNSQDPQNGVILDYELQYKEISEYNATA 485  
Db 461 SVNITTTQAAPSPVTVNKKGKIAKNSISLSQWEPDRNGIILEYKFEK-QETSVTI 519  
Qy 486 IKSPNTVTVOGLKAGAIYFQVQARTVAGYGRYSGKMYFQTMTEAEYQTSIQBKPLII 545  
Db 520 IKSKETTITAEGLKAPSVYFQIBARTAAAGYGFSPRFEFET-TPVFGASNDQSQIPIIG 578  
Qy 546 GSSAAGLVFLIAVVIAVCNRRGFERADSEYTDKLOHTYSGHM-TPGMKIYIDPFTYED 604  
Db 579 VSVTVGVILL--AVMIGFLRRCYGRSKAQDPEBEKWHFHNGHILKPGVRTYIDPFTYED 636  
Qy 605 PNEAVREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKOR 664  
Db 637 PTQAVHEFGKEIBASCITISERVIGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKOR 696  
Qy 665 RDLSEASIMQGFDPHNVHLEGVVTKSTPMIITEFMENGSLDSFLRQNDGQFTYOLV 724  
Db 697 RDLSEASIMQGFDPHNIHLEGVVTKSTPMIITEFMENGSLDTFLKXNDGQFTYOLV 756  
Qy 725 GMLRGIAGKYLADNMYVHRDLAARNILVNSNLVCKVDSFGLSRFLDSDTPTYSAL 784  
Db 757 GMLRGIAGKYLSDMGVHRDLAARNILVNSNLVCKVDSFGLSRFLDSDTPTYSAL 814  
Qy 785 GGIPIRTWTAPEAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMTNQDVINAIEQDYR 844  
Db 815 GGIPIRTWTAPEAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMTNQDVINAIEQDYR 874  
Qy 845 LPPMDCPSALHQLMCDQKDRNHRPKFGQIVNTLDMKIRNPNLSLKAMAPLSSGINLPL 904  
Db 875 LPSMDCPSALYQLMCDQKDRNHRPKFGQIVNTLDMKIRNPNLSLKAMAPLSSGINLPL 934  
Qy 905 LDRITPDYTSNTVDEMLEAKMCKQYKESFANAGTSPDVVSOMME 951  
Db 935 AEHSGSGAYRSVGEWLEATKMGRYTEIFMENGYSSMDAVAQVTL 981

RESULT 18  
B45583  
receptor tyrosine kinase Cek4 - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: B45583  
R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.  
New Biol. 3, 769-778, 1991  
A;Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse and rat.  
A;Reference number: A45583; MUID:92031278; PMID:1657122  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-983 <SA>  
A;Cross-references: UNIPROT:P29318; GB:M68514; NID:9454809; PIDN:AAA48666.1; PID:9211447  
A;Note: sequence extracted from NCBI backbone (NCBI:62405, NCBI:62411)  
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein  
F;619-895/Domain: protein kinase homology <KIN>  
F;627-635/Region: protein kinase ATP-binding motif

Query Match 56.5%; Score 2931; DB 2; Length 983;

Best Local Similarity 56.2%; Pred. No. le-126;  
Matches 552; Conservative 178; Mismatches 233; Indels 20; Gaps 9;  
Qy 1 MALRRLLCAALLLLPLAA-----VEETLMDSTTATAELGMVHPPSPGWEVSGVDEN 52  
Db 1 MDRLRLDLLLLCAALGAGRLSARPGNEVLLDSKTIQGLGWLISYFSGHWEISGVDEH 60  
Qy 53 MNTIRTYQVCNVPSESSQNNWLRTKFIIRRRGAHRIHVMKFSVRDCSSIPSVPSCKETFN 112  
Db 61 YTPIRTYOESNVMDHSQNNWLRTNWI PRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFN 120  
Qy 113 LYIYEAQFDSATKTFPMNMPNPKVVDITIAADSFSDVLDGGRVMKINTVRSFGPVRS 172  
Db 121 LYIMESDDDLHLAK----FREHQFTKIDTIAADESFTQMDLGRDLKLTNTEVREVPVSK 176  
Qy 173 GFYLAFODYGGCSLIIAVRVPRKCPRIIONGAIFQETLSGAESTLSVAARGSCIANAE 232  
Db 177 GFYLAFODVGCACVALSVRVYFKCPTVKNLAMPDTPV-MDSQSLVVEVGVSCVNSKE 235  
Qy 233 VDVPILKLYCNGDGEWLVPICRMCKAGFAVENGTGRCGPGSTGFKANQGDDEACTHCPIN 292  
Db 236 EEPK-KMYCSTEGEWLVPIGKCLCNAGYE--ERGFACQACRPGYKASAGNVKCAKCPH 292  
Qy 293 SRTTSEGATNCVCRNGYRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPRDSGG 352  
Db 293 SSTYEDASLNCRCENYFRSEKDPSPMACTRPPSAPRNVISNINETSIVLDSWPLDTGG 352  
Qy 353 REDLVNIIKSCGSGRGACTRCGDNVQAPROLGLTEPRIYISDLAHTQYTFEIOAVN 412  
Db 353 RKDVTNIIKCKGGSSKICEPCSDNVRFLPRTGLTNTVTVVVDLHAHTNYTFEIDA 412  
Qy 413 GVTDSQSPSPQFASVNTTQAAPSASVIMHQSRTVDSITLSNSQDPQNGVILDYELQ 472  
Db 413 GVSDDLSTLSRQFAAVSITTTQAAPSPTIVIRKORTSRNSVLSWQEPHEHNGIILDEVK 472  
Qy 473 YKEKELSEYNATAIKSPNTVTVOGLKAGAIYFQVQARTVAGYGRYSGKMYFQTMTEAE 532  
Db 473 YKEKQEOETSYTLRAKSTNTVTSGLKPDPTTYFQIPARTAAARYGTSSRPFEPETSPDS- 531  
Qy 533 YQTSIQBKPLIIIGSSAAGLVFLIAVVIAVCNRRGFERADSEYTDKLOHTYSGHM-TP 591  
Db 532 FSTSSSENQVVMIAISAIAVAIIILTVVYVYVIGRFGCYKSKGKTDEKRLFHNGHILKLP 591  
Qy 592 GMIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRKEIFVA 651  
Db 592 GLRTYVDPTHYEDPNQAVHEFAKELDASNISIDKVVGAGFGEVCSGRLKLPKKEISVA 651  
Qy 652 IKTLKSGYTEKORRDLSEASIMQGFDPHNVHLEGVVTKSTPMIITEFMENGSLDSFL 711  
Db 652 IKTLKAGYTEKORRDLSEASIMQGFDPHNIHLEGVVTKSTPMIITEFMENGSLDSFL 711  
Qy 712 RQNDGQFTVQLVGLMRLGIAAGKYLADNMYVHRDLAARNILVNSNLVCKVDSFGLSRFL 771  
Db 712 RKHDAQFTVQLVGLMRLGIAAGKYLSDMGVHRDLAARNILVNSNLVCKVDSFGLSRFL 771  
Qy 772 EDTSDPTYSALGKGIPIRTWTAPEAIQYRKFTSASDVWSYGIWMVMSYGERPYWDMT 831  
Db 772 EDD-PEAAVYTR-GGIPIRTWTSPEALAYRKFTSASDASVSGIWLVEWMSYGERPYWEMS 829  
Qy 832 NQDVINAIEQDYRLPPMDCPSALHQLMCDQKDRNHRPKFGQIVNTLDMKIRNPNLSLK 891  
Db 830 FQDVIRKAVDEGYRLPPMDCPSAALYQLMCDQKDRNHRPKFGQIVNTLDMKIRNPNLSLK 889  
Qy 892 AMAPLSSGINLPLDRTIPDYTSNTVDEMLEAKMCKQYKESFANAGTSPDVVSOMME 951  
Db 890 IITNAARPNLLDQSNIDISAFRTAGDMLNGFRTGQCKGIFTGVYSSCDTIKISTD 949  
Qy 952 DILRLGVTLAGHQKILNSIQVM 974  
Db 950 DMKKVGTVVVGPKKIVSSIKTL 972

RESULT 19



616 LDATNISIDKVVGGAGEFGEVCSGRLKLPSSKEISVAIKTLKVGYTEKQRDPFLGEASIMG 676

676 QFDHNPIVHLRGVVTKSPVPMIITEFMENGSLDSFLRQNDGQFTVQLVGLRGIAGAGMK 735

676 QFDHNPIVHLRGVVTKSPVPMIITEFMENGSLDSFLRQNDGQFTVQLVGLRGIAGAGMK 735

736 YLADMMYVHRDLAARNILVNSNLVCKVSDRGLSRFLIEDTSDPTYSALGGKIPIRWTAP 795

736 YLSDMGYVHRDLAARNILVNSNLVCKVSDRGLSRVLEDD-PEAAYITR-GGKIPIRWTSP 793

796 EAIQYRKFTSASDWSYGI VNMVWYSYGERPYDMTNDQDVINAIEDQYRLPPMDCPSAL 855

794 EAIYRKFTSASDWSYGI VLVWVWYSYGERPYWMSNQDVIKAVDEGYRLPPMDCPAAL 853

856 HQMLDCWQKDRHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPILDRTPIDYTSF 915

854 YQLMLDCWQKDRHRPKFEQIVSLDLKLRNPGSLKIITSAARPSNLLDDQSNVDISTP 913

916 NTVDWELAIKMGQYKESFANAGPSTSFDVVSQMMMEDILRLGVLTLAGHQKILNSIQVNR 975

914 RTTGDWLVNGVRAHCKEIFTGVYSSCDTIAKISTDDMKVGVTVVGPQKKIISSIKALE 973

976 AQ 977

974 TQ 975

RESULT 20

S49015

receptor tyrosine kinase Etk-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004

C:Accession: S49015; S51602

R:Maisionpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.

Oncogene 8, 3277-3288, 1993

A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine

A:Reference number: S49015; MUID: 94067777; PMID: 7504232

A:Accession: S49015

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1005 <NAI>

A:Cross-references: UNIPROT:P54757; EMBL:S68024

A>Note: the authors translated the codon GAC for residue 170 as Glu

A:Accession: S51602

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-305, 'G', 359-1005 <MA2>

A:Cross-references: EMBL:S68026

A>Note: the authors translated the codon GAC for residue 170 as Glu

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type I

C:Keywords: ATP; transmembrane protein

F:675-941/Domain: protein kinase homology <KIN>

F:683-691/Region: protein kinase ATP-binding motif

Query Match 56.3%; Score 2923; DB 2; Length 1005;

Best Local Similarity 57.2%; Pred. No. 2.4e-126; Indels 36; Gaps 1

Matches 555; Conservative 161; Mismatches 218;

Qy 6 LGCAALLPLLAAREETLMDSTTATBLGMVHPHPPSGWEEVSGYDENMNTITTYQVCNVF 65

Db 48 LCAALRTLLASPSNEVNLDSRTVLGLGWIAFPKNGWEIGVEDENYAIPTTYQVCVM 10

Qy 66 ESSQNWLRTFIRRRGNHRHIVEMKESVDCSSIPVSGCKETENLYYYEADPDSATK 12

Db 108 EQQNQLLTWISNEGASRIFILSKETLRKDCNSLPGGLGTCKETENMYFESDDENG- 16

Qy 126 TFPNWMENPWKVDITIADESFSQVDLGGRVKMLNTEVRSFGVPSRGYFLAFQYGGCM 18

Db 167 ---NIKONQYIKIDITIADESFTELDLGDRVMKLNTEVRDVGFLSKGFLYAFQDVGACI 22

Qy 186 SLIAVVFYKCPRIIONGALFOETLSCAGSTSLVAARGSCIANAEVDVPKLYCNGDG 24





mouse developmental kinase 2 (MDK2) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: 148652  
R:Clousek, T.; Lerch, M.M.; Ullrich, A.  
Oncogene 11, 2085-2095, 1995  
A:Title: Cloning, characterization, and differential expression of MDK2 and MDK5, two novel members of the mitogen-activated protein kinase family  
A:Reference number: 148652; MUID:96074837; PMID:7478528  
A:Accession: 148652  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-987 <RES>  
A:Cross-references: UNIPROT:P54761; EMBL:Z49085; NID:g1089897; PIDN:CAA89909.1; PID:g1089897  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat domain  
C:Keywords: ATP; transmembrane protein  
F:322-417/Domain: fibronectin type III repeat homology <FN3A>  
F:433-518/Domain: fibronectin type III repeat homology <FN3B>  
F:613-881/Domain: fibronectin type III repeat homology <KIN>  
F:621-629/Region: protein kinase ATP-binding motif  
F:904-970/Domain: SAM homology <SAM>

Query Match 55.0%; Score 2854.5; DB 2; Length 987;  
Best Local Similarity 56.4%; Pred. No. 3.2e-123;  
Matches 552; Conservative 159; Mismatches 251; Indels 17; Gaps 10;

QY 6 LGAALLPLLAAYVEETLMDSTTATAGLGMVHPPS--GWEVSGYDENMNTIRTYQVCN 63  
DB 3 LRALLCWASLATALEETLNTKLETADLKWTYTPQAGQWEEELSGLEQHSVRTYEVC 62  
QY 64 VPE-SSQNNWLTFRIRRGAAHIVEMKFSVRDCSSIPSPVSGCKETFLNYIYEAEDFS 122  
DB 63 MKRPGQGAHURKWTGVPVRRGAVHVATIRFTMECLSLPRASRSCKETFTVFYIESERD 122  
QY 123 AKTTPFNWENPWVKVDITIADESPQVDLGRVNMKINTEVRSFGVSRSGFYLAPODYG 182  
DB 123 ATAHTPAMNENFYIKVDIVAAEHLTRKPRGAETGKNIKITRLGLPSLKAGFYLAPODQ 182  
QY 183 GMSLIATVFRKCPRIIONGAIFQETLSGAESTSLVAARGSCITANAEEDVPI-KLYC 241  
DB 183 ACWALLSLFLFKKCSWLTNTIYTFEIV---PRELVFVAGSCVANAAPVTPANSPSLYC 239  
QY 242 NGDGEWL-VPIGRCKMCKAGFEAVENGTCVRCGSCGTFKANQGDCACTHCPINSTRTEGA 300  
DB 240 REDGQWAEQVTCGSCAPGFAEAEKVKCRACGQGTFFKQIGDSCILPCPANSHNNIGS 299  
QY 301 TNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGREDLVNI 360  
DB 300 FVCLCRIGYRARSPPRSFCTTPPSAPRSVVHLLNGSTLRLEWAPLESGERDLTYAV 359  
QY 361 ICKSCGSGRACGTRCGDNVOYAPRQLGLTEPRIVYSDLIATQYTFEIQAVNGVTDQSPF 420  
DB 360 RCRECRPG-GSCLPCGDMTFPGPRDLVEPVAIRGLRDPVYTFEVAALNGVSTLATG 418  
QY 421 SPQFASVNTTNOAAPSAVSMHQSRTVDSITLWSQPDQNGVILDYELQYKEKELSE 480  
DB 419 PPPEPVNVTDEVPVAVSDIRVTRSSPSLISWAIAPRASPAGVLDYEVYKHEKGAEG 478  
QY 481 YNATA-IKSTNTVTVOGLKAGAIYVQVARTVAGYGRYSGVMYFQT-MTEABYQTSIQ 538  
DB 479 PSSVRFLKTSNRAELRGLRGASLYLVQVRAEAGYFGQEHHSQTLQDSE---SWR 535  
QY 539 EKLPLIIGSAAAGFLIIVVIAIVCNRRGRFERADSEYTDKLQHYTSGMTPGMKIYID 598  
DB 536 EQALLAGTAVGVLVVLVVVIAVLCLRKQSGREVEYSDKHGQVLIH---GTRKVYID 592  
QY 599 PFTYEDNEAVREFAKEIDISCVKIQVITGAGFGEVCSCHLKLCKRIFVAIKTLKSG 658  
DB 593 PFTYEDNEAVREFAKEIDISYVKIEVIGAGFGEVCRGLKAPKCKSCVAIKTLKGG 652  
QY 659 YTEQRDRFLSEASIMQFDPHPNVHLEGVVTVKTSTFVMIITEFMENGLSDSLRQNDQGF 718  
DB 653 YTEQRDRFLSEASIMQFDPHPNIRLEGVVTNSVFMILTEFMENGALDSLRLRNDQGF 712

QY 719 TVIQLVGLRGIAAGMKYVLADMYVHRDLAARNILVNSNLVCKVSDPGLSRFLEDDTSDP 778  
DB 713 TVIQLVGLRGIAAGMKYLAEMSVYHRDLAARNILVNSNLVCKVSDPGLSRFLEENSSDP 772  
QY 779 TYSALGGKIPIRWTAPEAIQYRKFTSASDVWSYGIYVWEVMSYGERPYKMDTNOOVINA 838  
DB 773 TYSALGGKISIRWTAPEAIQYRKFTSASDAWSYGIYVWEVMSYGERPYKMDTNOOVINA 832  
QY 839 IEQDYRLPPMDPCSAHQMLDCQKDRNHRPKFGIVNTLDKWIIRNPNSLKAMAPLSS 898  
DB 833 IEQDYRLPPMDPCPTSLHQLMDCQKDRNARFRFPQVVSALDKWIIRNPNSLKIVARENG 892  
QY 899 GINPLDRTTIDPTYSFNTVDENLEAKMGQYKESPANAGFTSPDVVSQMMEDILRLV 958  
DB 893 GASHELLDQRPYSAFSGVGEMLRAIKMGRYEESFAAGFSGFEVVSQISAEDLLRIGV 952  
QY 959 TLAGHOKILANSIQVMRAQ 977  
DB 953 TLAGHOKILANSIQVMRAQ 971

RESULT 23  
AS4092  
protein-tyrosine kinase (EC 2.7.1.112) htk precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Aug-1994 #sequence\_revision 02-Aug-1994 #text\_change 09-Jul-2004  
C:Accession: AS4092  
R:Bennett, B.D.; Wang, Z.; Kuang, W.J.; Wang, A.; Groopman, J.E.; Goeddel, D.V.; Scadden  
J. Biol. Chem. 269, 14211-14218, 1994  
A:Title: Cloning and characterization of HTK, a novel transmembrane tyrosine kinase of the  
A:Reference number: AS4092; MUID:94245746; PMID:8188704  
A:Accession: AS4092  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-987 <BEN>  
A:Cross-references: UNIPROT:P54760; GB:U07695  
C:Genetics:  
A:Gene: GDB:HTK  
A:Cross-references: GDB:362753; OMIM:600011  
A:Map position: 7pter-7qter  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat domain  
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase  
F:433-518/Domain: fibronectin type III repeat homology <3FR>  
F:613-881/Domain: fibronectin kinase homology <KIN>  
F:621-629/Region: protein kinase ATP-binding motif  
F:904-970/Domain: SAM homology <SAM>

Query Match 54.8%; Score 2844; DB 2; Length 987;  
Best Local Similarity 56.0%; Pred. No. 9.5e-123;  
Matches 553; Conservative 160; Mismatches 247; Indels 28; Gaps 13;

QY 1 MALRRGAALLPLLAAYVEETLMDSTTATAGLGMVHPPS--PSGWEVSGYDENMNTIR 58  
DB 1 MELRVL---LCWASLATALEETLNTKLETADLKWTYTFEIVQVDGQWEEELSGLEQHSVRT 57  
QY 59 YQVCNFPES-SQNNWLTFRIRRGAAHIVEMKFSVRDCSSIPSPVSGCKETFLNYIY 117  
DB 58 YEVCDVQARQGAHLETLGVPVRRGAVHVATIRFTMECLSLPRAGRSCKETFTVFY 117  
QY 118 ADPDSATKTPFNWENPWVKVDITIADESPQVDLGRVNMKINTEVRSFGVSRSGFYLA 177  
DB 118 SDADTATALTAPMENENFYIKVDIVAAEHLTRKPRGAETGKNVKTIRLGLPSLKAGFYLA 177  
QY 178 FQDYGGMCSLIATVFRKCPRIIONGAIFQETLSGAESTSLVAARGSCITANAEEDVPI 237  
DB 178 FQDYGGMCSLIATVFRKCPRIIONGAIFQETLSGAESTSLVAARGSCITANAEEDVPI 234  
QY 238 -KLYCNGDGEWL-VPIGRCKMCKAGFEAVENGTCVRCGSCGTFKANQGDCACTHCPINSTR 295  
DB 235 PSLYCREDGQWAEQVTCGSCAPGFAEAEKVKCRACGQGTFFKPLSGEGSCQPCPANSHS 294  
QY 296 TSEGATNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGRED 355  
DB 296 TSEGATNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGRED 355

Db 295 NTIGSAVQCVRGVFRARTDPRGAPCTTPPSAPRSVVRSLNGSLHLWESAPLESQGRD 354  
Qy 356 LVYNIICKSGRGACTCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGV- 414  
Db 355 LTALRCRCRPG-GSCAPCGDLTFDPPDLVPPVVRGLRPPDTYTFEVALNGVS 413  
Qy 415 ---TDGSPFPQFASVNTTQAAPSASIMHQVSRVTSITLSWSQDPQNGVILDYEL 471  
Db 414 SLATGPVPPFP---VNVVTTDREVPVAVSDIRVTRSSPSLSLAWAVPRAPSGAVLDYEV 469  
Qy 472 QYVEKELSEYNATA-IKSPNTVTVOGLKAGAIYVFOVARTVAGYGRYSKMYFOT-MT 529  
Db 470 KYHEKAGBSSVRFLTSNRAELGLKRGASLYVQVARSAGYFPFQEHHSQTOLD 529  
Qy 530 EASYQTSIQEKLPLIIGSSAAGLVFLIAVVVIAIACVNRGFRADSEYTDKLOHYTSGHM 589  
Db 530 ESE---GWRQALALACTAVGVVVLVAVVAVLCLRKQSGREAEYSKDGQYLIGH- 585  
Qy 590 TPGMKYIDPFTEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIF 649  
Db 586 --GTVKYIDPFTEDPNEAVREFAKEIDVSYYKIEEVIGAGEFGEVCRGLKAPGKESC 643  
Qy 650 VALKTLKSGYTEKORRDFLSEASTMGOFDPHPNVTHLEGVVTKSTPVMIIIFERMENGLSDS 709  
Db 644 VALKTLKGGYTEKORRDFLSEASTMGOFDPHPNVTHLEGVVTKSTPVMIIIFERMENGLSDS 703  
Qy 710 FLRQNDQFTVIOVLGMLRGIAAGMYLADNVYVHRDLAARNILVNSLVCKYSDFGLSR 769  
Db 704 FLRLNDQFTVIOVLGMLRGIAAGMYLADNVYVHRDLAARNILVNSLVCKYSDFGLSR 763  
Qy 770 FLEDDTSDPTYSALGKGIPIRTAPEAIQYRKFTSASVWSYGIYVMEVMSYGERPYWD 829  
Db 764 FLENSSDPTYSALGKGIPIRTAPEAIQYRKFTSASVWSYGIYVMEVMSYGERPYWD 823  
Qy 830 MTQNDVINAIEQYRLPPPPDCPTSLHQLMDCWKDRNHRPKFGQIVNTLDKMRNPNS 889  
Db 824 MSNDVINAIEQYRLPPPPDCPTSLHQLMDCWKDRNHRPKFGQIVNTLDKMRNPNS 883  
Qy 890 LKAMAPLSSGINPLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGTSPDVVSQMM 949  
Db 884 LKIVARENGASHPDLLDQRPVSAFSGVGEWLAIRKMGRYESFAAAGFSGFELVSQIS 943  
Qy 950 MEDILRGVTLGAGHKKILNSIQVMAQ 977  
Db 944 AEDLLRIGVTLGAGHKKILASVQHMSQ 971

RESULT 24  
148953  
eph-related receptor protein tyrosine kinase - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48953  
R;Andres, A.C.; Reid, H.H.; Zurcher, G.; Blaschke, R.J.; Albrecht, D.; Ziemiacki, A.  
Oncogene 9, 1461-1467, 1994  
A;Title: Expression of two novel eph-related receptor protein tyrosine kinases in mammary  
A;Reference number: I48953; MUID:94203677; PMID:8152808  
A;Accession: I48953  
A;Status: preliminary; translated from GH/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-987 <RES>  
C;Cross-references: UNIPROT:P54761; EMBL:U06834; NID:9459172; PIDN:AAA18591.1; PID:94591  
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
C;Keywords: ATP; transmembrane protein  
F;322-417/Domain: fibronectin type III repeat homology <FN3A>  
F;433-518/Domain: fibronectin type III repeat homology <FN3B>  
F;613-881/Domain: protein kinase homology <KIN>  
F;621-629/Region: protein kinase ATP-binding motif  
F;904-970/Domain: SAM homology <SAM>

Query Match 54.2%; Score 2811.5; DB 2; Length 987;  
Best Local Similarity 55.8%; Pred. No. 2.9e-121;  
Matches 545; Conservative 159; Mismatches 256; Indels 17; Gaps 10;

Qy 6 LGAALLPLLAAVEETLMDSTTATAELGWMVHPPS--GWEEVSGYDENNTIRTYQVCN 63  
Db 3 LRALLCWASLATALEETLLNTKLETADLKWVTPYQAEQWHEELSGLEQHSVRYTEVCD 62  
Qy 64 VFE-SSONNLWRTKFTIRRGARHIVEMKFSVRDCSSIPSPVSGCKTFLNLYYEAFDPS 122  
Db 63 MKRPGGQHLWRTGWPRRGAVHYATIRFTMMECLSLPRASRCKETFTVFVYESRDT 122  
Qy 123 ATKTFENMNPVVKYDVTIAADESFQVDLGGVRMKINTVRSFGVSRSGFYLAFOYDYG 182  
Db 123 ATAHTFAMMENFYKVDTVAAEHLTKRPGAEATGKVNIIKTLRGLPSKAGFYLAFOOQG 182  
Qy 183 GCMSLIAVRFYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAAEVDVPI-KLYC 241  
Db 183 ACWALLSLHLFYKCSWLIITNLTYFPETV---PRELVVPVAGSCVANAAPTANPSPLYC 239  
Qy 242 NGDGEWL-VPIGRCMKAGFEAVENGTVCRGCSPTFKANQGDCACTHCINSRTTSEGA 300  
Db 240 REDGQWABQQVTCSCAPGYEAAESNKKVCRACQGTFPKQIGDESLCPCPANSHNNGS 299  
Qy 301 TNCVCRNGYVRADLDPLDMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDGGREDLVYNI 360  
Db 300 PVCLCRIGYTRASDRSPSPCTTPPSAPRSVVRHLNGSTLRLEWSAPLESGRPDLYAV 359  
Qy 361 ICKSCSGRGACTCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPF 420  
Db 360 RCRECRPG-GSCLPCGDMTDFPGPDLVERWVAIRGLRPDVTYTFEVAALNGVSTLATG 418  
Qy 421 SPOFASVNTTQAAPSASIMHQVSRVTSITLSWSQDPQNGVILDYELQYVEKELSE 480  
Db 419 PPPFPVNTTDEVPVAVSDIRVTRSSPSLSLAWAPRAPSGAVLDYEVKYEKAGG 478  
Qy 481 YNATA-IKSPNTVTVOGLKAGAIYVFOVARTVAGYGRYSKMYFOT-MTEAEYQTSIQ 538  
Db 479 PSSVRFLKTSNRAELRGLKRGASLYVQVARSAGYFPFQEHHSQTOLDSE---SWR 535  
Qy 539 EKLPLIIGSAAGLVFLIAVVVIAIACVNRGFRADSEYTDKLOHYTSGHMTPGMKYIID 598  
Db 536 EQALLAGTAGVGVVLVAVVIAVLCRKQSGREVEYSDKHGQYLIGH---GTVKYIID 592  
Qy 599 PFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTKSG 658  
Db 593 PFTYEDPNEAVREFAKEIDVSYYKIEBEVIGAGEFGEVCRGLKAPGKESCAVKTLKGG 652  
Qy 659 YTEKORRDFLSEASTMGOFDPHPNVTHLEGVVTKSTPVMIIIFERMENGLSDSFLRNDQGF 718  
Db 653 YTERQRAEFLSEASTMGOFDPHPNVTHLEGVVTKSTPVMIIIFERMENGLSDSFLRNDQGF 712  
Qy 719 TVIQLVGLRGIAAGMYLADNVYVHRDLAARNILVNSLVCKYSDFGLSRFLDDTSDP 778  
Db 713 TVIQLVGLRGIAAGMYLADNVYVHRDLAARNILVNSLVCKYSDFGLSRFLDDTSDP 772  
Qy 779 TYTSALGKGIPIRTAPEAIQYRKFTSASVWSYGIYVMEVMSYGERPYDMTQDVINA 838  
Db 773 TYTSALGKGIPIRTAPEAIQYRKFTSASVWSYGIYVMEVMSYGERPYDMTQDVINA 832  
Qy 839 IEODYRLPPMDPCPSALHQLMDCWKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSS 898  
Db 833 IEODYRLPPMDPCPSALHQLMDCWKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSS 892  
Qy 899 GINPLDRTTIPDYTSFNTVDEWLEAIKMGQYKESFANAGTSPDVVSQMMEDILRGV 958  
Db 893 GASHPLDQRPVSAFSGVGEWLAIRKMGRYESFAAAGFSGFEMVYSQISAEALLRIGV 952  
Qy 959 TLAGHOKKILNSIQVMAQ 975  
Db 953 TLAGHOKKILASVQHMSQ 969

RESULT 25  
150617  
protein-tyrosine kinase (EC 2.7.1.112) Cek8 - chicken (fragment)

C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50617; S33505  
R:Sajjadi, F.G.; Pasquale, E.B.  
Oncogene 8, 1807-1813, 1993  
A:Title: Five novel avian Eph-related tyrosine kinases are differentially expressed.  
A:Reference number: I50611; MUID:93288394; PMID:8510926  
A:Accession: I50617  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-849 <SAJ>  
A:Cross-references: UNIPROT:Q07496; EMBL:Z19059; NID:g312216; PIDN:CAA79509.1; PID:g31222  
C:Gene: Csk8  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: S51605  
R:Maisonpierre, P.C.; Barrezuela, N.X.; Yancopoulos, G.D.  
Oncogene 8, 3277-3288, 1993  
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam  
A:Reference number: S49015; MUID:94067777; PMID:7504232  
A:Accession: S51605  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-948 <MAI>  
A:Cross-references: UNIPROT:P54758; EMBL:S68030  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
C:Keywords: ATP; transmembrane protein  
F:628-936/Domain: protein kinase homology <KIN>  
F:636-644/Region: protein kinase ATP-binding motif

Query Match 52.6%; Score 2728.5; DB 2; Length 849;  
Best Local Similarity 59.6%; Pred. No. 1.5e-117;  
Matches 512; Conservative 139; Mismatches 181; Indels 27; Gaps 9;

Qy 132 ENPWKVTDTAADSFSQVDLGRVMKINTEVRSFGVSRSGFLAFQDYGGWLSIAVR 191  
Db 2 ESOPAKIDTAADESFTQVDIGDRIMKLNTEVDRVGLSKKGFYAFQDVGACIALVSVR 61  
Qy 192 VFYKPCRIIONGAIFQETLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEVLVPI 251  
Db 62 VFYKCPILVNLAQFPDTTIGATDSSLVEVRGSCVNSEKQVP-RWYCGADGEVLVPI 120  
Qy 252 GRMCKAGFAVENGTWCRGCPSTFFKANQDEACTHCIPNSRTTSAGTNCVCRNGYR 311  
Db 121 GNCLNAGYE--ERNGEQACKIGYKALSTDVACAKCPHYSISWEGSTCTCDRFFR 178  
Qy 312 ADLQPLDMPCCTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVNIIKSCSGSRGA 371  
Db 179 AENDASMPCTRPPSAPQNLISNWNESVNLNENAPQNKGRDDISVNVCKRGAGEPS 238  
Qy 372 -CTRGGDNNQVAPRQLGTEPRIYISDLAHTQYTFEIQAVNGVTDGSPSPQASVNI 430  
Db 239 HCRSGSGVHSPQNGKLTTKVSTIDLLAHTNTFEVWAVNGVSKNPSQDQAVSVTV 298  
Qy 431 TNQAAPSASVIMHQVSRVDSITLSWSQDPQNGVLDLQYQYKELSEYNATAIKSPT 490  
Db 299 TNQAAPSPIALTOAKEITRHSVALAWLEPDRNGVILEYKYEKKOQNTYRIVKTAS 358  
Qy 491 NTVTVQGLKAGAIYVQVRAITVAGYGRYSGMVFQMTAEAYQTSIQEKL-----PLI 544  
Db 359 RNTDINGLNLPLTSYVPHVARTAGYGDPSGPFETNT-----VPSPIIGDTNPTV 411  
Qy 545 IGSSAAGLVFLIAVVVIAVNCNR--GPERADSEVTDKLQHYTSGHMTGPKMIYIDPETY 602  
Db 412 LLVSVAGSVLVVILIAAFVISRRSKYSKAKQEADEE-----KHLNQGVRTYVDPTY 465  
Qy 603 EDPNFAVREFAKEIDISCKVEQVIGAGEFGVCSGHLKLPGRIFVAIKTLKSGYTEK 662  
Db 466 EDPNQAVREFAKEIDASCIIKEKVIGVGEFGVCSGRLLKVPQKREICVAIKTLKAGYTDK 525  
Qy 663 QRDRFLSEASIMQDPDHPNVHLEGVTKSTPMIITEFMENGSLDSFLRQNDGQFTVIQ 722  
Db 526 QRDRFLSEASIMQDPDHPNI IHLEGVTKCKPMIITEFMENGSLDAFLRKNDGRFTVIQ 585  
Qy 723 LVGMURGIAAGKYLADMYVHRDLAARNILVNLVCKVDPGLSFLRDDTSDPTVTS 782  
Db 586 LVGMURGISGMYKLSYVHRDLAARNILVNLVCKVDPFGMSRVLEDD--PAAATY 644  
Qy 783 ALGGKPIRWTAPETAYQKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVINAQD 842  
Db 645 R-GGKPIRWTAPETAYKFTSASDVWSYGIWMEVMSYGERPYWDMNSQDVKAIBEG 703  
Qy 843 YRLPPPMDCPSALHQLMDCWQKDRNRPFGQIVNTLDKMTNPNLSLKAMAPLSGGINL 902

Db 704 YRLPPPMDCPTALHQLMDCWQKERSDRPKFGQIVNMLDKLRNPNLSLKRTGSSSRPST 763  
Qy 903 PLLDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGTSPDVVSQMMEDILRLGVLAG 962  
Db 764 ALLDPSSEFSAVSVSWDLQAIKMYKQNFYTAAGTYTLEAVVHMNQDDLARIGITAIT 823  
Qy 963 HOKKILANSIQVWRAQMNQI 981  
Db 824 HONKILSSVQAMRSQMQM 842

RESULT 26  
S51605  
receptor-like tyrosine kinase Etk-2 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: S51605  
R:Maisonpierre, P.C.; Barrezuela, N.X.; Yancopoulos, G.D.  
Oncogene 8, 3277-3288, 1993  
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam  
A:Reference number: S49015; MUID:94067777; PMID:7504232  
A:Accession: S51605  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-948 <MAI>  
A:Cross-references: UNIPROT:P54758; EMBL:S68030  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
C:Keywords: ATP; transmembrane protein  
F:628-936/Domain: protein kinase homology <KIN>  
F:636-644/Region: protein kinase ATP-binding motif

Query Match 50.1%; Score 2599.5; DB 2; Length 948;  
Best Local Similarity 53.1%; Pred. No. 1.3e-111;  
Matches 498; Conservative 147; Mismatches 225; Indels 67; Gaps 12;

Qy 13 LPLLAA-----VEETLMDSTTATAELGMVWHPSPSGWEVSGVDENMNTIRTYQVCN 63  
Db 17 LPLLTAWTGDCSHVSNQVLLDTSTVMGELGWKTYPLNGWDAITEMDENRRIHTYQVCN 76  
Qy 64 VFSSQNNMLRTKFIKRRGAHRIHVEMKFSVRDCSSIPVSGSCKETFLNYEADFSA 123  
Db 77 VMEPNQNNMLRTNWSIRSDAAQKIYEMKFTLRDCNSIPWVLGTCKETFTLYIESDESHG 136  
Qy 124 TKTFPNNMENPVKVDITIAADSFSQVDLGRVMKINTEVRSFGVSRSGFLAFQDYGG 183  
Db 137 TKFKP---SQYIKIDTIAADESFTQMDLGRILKLNTEVREVGPIERKGFYAFODIGA 192  
Qy 184 CMSLIAVRVYRCPRIIONGAIFQETLSGABSTSLVAARGSCIANAEVDVPIKLYCNG 243  
Db 193 CIALSVRVYRCKPFTVRNLAMFPDITIPRVDSLSLVEVRGSCVKSEERDTP-KLYCGA 251  
Qy 244 DGBWLVPIGRMCKAGFAVENGTWCRGCPSTFFKANQDEACTHCIPNSRTTSSEGTATNC 303  
Db 252 DGBWLVPLGRCICTTGVEELEGS--CHACRPGYKAPAGNTKCKSPHSSSTFEATSV 309  
Qy 304 VCRNGYVRADLDPLDMPCCTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVNIIK 363  
Db 310 HCEKGYFAEKDPPSACTRPPSAPRNVAFINETALILEWSPPSDTGGHKKDUTYSVICK 369  
Qy 364 SCGSGRGACTRCGDNQVQAPRQLGTEPRIYISDLAHTQYTFEIQAVNGVTDGSPSPQ 423  
Db 370 KCGVDASQCDGCGAGLAFIPRFGILNNSVVLDFVSHVNTYFIEAMNGVSELSIPKP 429  
Qy 424 FASVNTITNQAAPSASVIMHQVSRVDSITLSWSQDPQNGVLDLQYQYKELSE--Y 481  
Db 430 FTAITVTDDQDAPSLIGMWRKDWASQNSIALSQAFNSGAILDVEIKYEKEHEOLTY 489  
Qy 482 NATAIKSPFTVTVQGLKAGAIYVQVRAITVAGYGRYSGMVFQMTAEAYQTSIQEKL 541  
Db 490 SSTESKAP--SVIITGLKRPATTYFIHRVTAITAGYSGYSOKFFETGDETSDMAEQGI 547  
Qy 542 PLIIGSSAAGLVFLIAVVVIAVNCNR--RGPERADSEVTDKLO-HYTSGHMT-PGMKIYID 598



Qy	6	LGAALLPLLAABEETLMDSTTAAELGWMVPPSGWEVSGYDENMTTIITYQVNVF	65
Db	48	LCAALRTLLASPSNEVNLDSRTVLGDLGFIAPKNGWEBIEGVDFNAPAIHTYQVCKVM	107
Qy	66	ESSQNNWLTKEFIRRGAAHRTHEVMKFSVRDCSSIPSPGSKETENLYYYEADPDSATK	125
Db	108	EQQNNWLTUSWISNEGASRPIELKFTLRDCNSLPGGLGCKETFNWYFSSDDENGR	166
Qy	126	TFPNMNMENPWKVDTTIAADESFQVDLGGRRVMKINTEVRSFGVPSRSGFYLAFOYGGOM	185
Db	167	--NIKQNOYIKIDTTIAADESFTELDLGDRLVMKLNTEVRDVGSLSKGFFYLAFOVGCACI	223
Qy	186	SLTAVRVFYKRCPRJLQNGALFOETLLSGAESTSLVAARGSCIANABEVDVPIKLYCNGDG	245
Db	224	ALVSVRVYIKKCPSVYRHUAVPDDITIGADSSQLLEVSGCV_NHVSVDTPDKMCHCSABG	282
Qy	246	EMLVPIGRCMCKAGFEAVENGTVRCGPSPGTFKANQGDDEACTHCPINSTRTSEGATNCVC	305
Db	283	EMLVPIGKCMCKAGYEE_KNGT_CQVCRPGFFKASPHSQTCSKCPHSHYTHEEASTSCVC	340
Qy	306	RNGYVBAADLDPLMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSC	365
Db	341	EKDYFRRESDDPTMACTT	358
Qy	366	GSRGACRTRCGDNQVYAPRQLGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPSPQPA	425
Db	359	----	358
Qy	426	SVNITTNQAAPSASVIMHOVSRTVDISITLSWSQDPQNGVILDYELQYBEKELSEYNATA	485
Db	359	-----PSPVTNVKKGKIAKNSISLSHQEPDRPNGIILEVIKYFEKD_QETSYTI	407
Qy	486	IKSPNTNVTVOGLKAGAIYVFOVRARTVAGYGRYSGKMVFQTMTEABYQTSIOEKUPLII	545
Db	408	IKSKETTITABGLKPPASVYVFOIRARTAGYGVFSRRFEFET_TPVFGASNDOSQIP-II	465
Qy	546	GSSAAGLVLIAVWIAIV-----CNR-----GFERADSEYTDKLO	582
Db	466	GVSVTVGVILLAVMIGFLSGSCCGGRASSLCANVHPSLIWRCGYSAKQDPBEEKM	525
Qy	583	HYTSGHM_TPGMKIYIDPPTYEDPNABVREFAKEIDISCVKIROVIGAGFEGVCSGHUK	641
Db	526	HFHNGHIKLPGVRTYIDPPTYEDPTQAVHEFGFKETIEASCITIERVIGAGFEGVCSGRUK	585
Qy	642	LPKREIFVAITKLSGYTEKORRDFLEASIMGQFDHPNVHLEGVVTKSTPVMIIITEF	701
Db	586	LPKREILPVAITKLVGYTEKORRDFLEASIMGQFDHPNIIHLEGVVTKSKPVMIVTEY	645
Qy	702	MENGLSDSFLRQNDGQFTVIQLVGLMRGIAAGMKYLDMMNVYHRDLAARNILVNSNLVCK	761
Db	646	MENGLSDTFLKNDGQFTVIQLVGLMRGIAAGMKYLSDMGVYHRDLAARNILINSNLVCK	705
Qy	762	VSDPGLSRFLEDDTSDPTVTSALGGKIPIRWTAPAIAOYRXKFTSASDWSYGVIMMEVMS	821
Db	706	VSDPGLSRVLEDD_PPAAYTTR_GGKIPIRWTAPAIAIAFRKFTSASDWSYGVIMMEVMS	763
Qy	822	YGERPYWDMTNQDVINAIBODYRLPPEPMDPCSAHLQMLMDCWQKDRNHRPKFGQIVNTILD	881
Db	764	YGERPYWEMTNQDVIXAVBEGYRLPSPMDCPAALYQLMLDCWQKDRNSRPKFDIVNMLD	823
Qy	882	KWIENPNSLKAMAPLSSGNILPLDRTIPDYSFNTVDWLEAIKMGQYKESFANAGFTS	941
Db	824	KLIIRNPSSLKTLINASSRSVSTLLAEHSGSLGSGAYRSVGEWLEATKMGRYTEIFMENGYS	883
Qy	942	FDVYSQMMME	951
Db	884	MDAVAQVTL	893

C>Date: 05-Jan-1996 #sequence revision 05-Jan-1996 #text\_change 09-Jul-2004

C/Accession: A571174; S233622; S40294; PNO547  
R/Saito, T.; Seki, N.; Matsuda, Y.; Kitahara, M.; Murata, M.; Kanda, N.; Nomura, N.; Yama  
Genomics 26, 382-384, 1995

A/Title: Identification of the human ERK gene as a putative receptor tyrosine kinase and  
A/Reference number: A57174; MUID:95324932; PMID:7601466

A/Accession: A57174  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-478 <SAI>  
A/Cross-references: UNIPROT:P29323; GB:D37827; NID:g1060894; PIDN:BAA07073.1; PID:g1060894

R/Chan, J.; Watt, V.M.  
Oncogene 6, 1057-1061, 1991

A/Title: erk and erk, new members of the eph subclass of receptor protein-tyrosine kinase  
A/Reference number: S23361; MUID:91296384; PMID:1648701

A/Accession: S23362  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 144-154, 'N', 156-204 <CHA>  
A/Cross-references: EMBL:X59292

R/Watt, V.M.  
submitted to the EMBL Data Library, May 1991

A/Reference number: S40294  
A/Accession: S40294  
A/Molecule type: mRNA  
A/Residues: 144-204 <WAT>  
A/Cross-references: EMBL:X59292; NID:g31222; PIDN:CAA41981.1; PID:g31223

R/Iwase, T.; Tanaka, M.; Suzuki, M.; Naito, Y.; Sugimura, H.; Kino, I.  
Biochem. Biophys. Res. Commun. 194, 698-705, 1993

A/Title: Identification of protein-tyrosine kinase genes preferentially expressed in emb  
A/Reference number: PNO547; MUID:93343925; PMID:7668222

A/Accession: PNO547  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 132-162, 'R', 164-478, 'X' <IWA>  
A/Cross-references: DDBJ:D14717

C/Genetics:  
A/Gene: GDB:ERK  
A/Cross-references: GDB:128637; OMIM:176946

A/Map position: lp36.1-lp36.1  
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
C/Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kin  
F:111-379/Domain: protein kinase homology <KIN>  
F:119-127/Region: protein kinase ATP-binding motif  
F:402-468/Domain: SAM homology <SAM>

## RESULT 29

A57174  
protein-tyrosine kinase (EC 2.7.1.112) erk - human (fragment)  
C:Species: Homo sapiens (man)



**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 16:41:06 ; Search time 41 Seconds  
(without alignments)  
1594.867 Million cell updates/sec

Title: us-09-914-883-2  
Perfect score: 5188  
Sequence: 1 MAURRIGALLLLPLLAWE.....ILNSIQVMRAQMNIQSVEV 986

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	5130	98.9	994	3	US-08-542-635-2
2	5093	98.2	970	2	US-08-449-645A-11
3	5093	98.2	970	2	US-08-702-367A-11
4	5093	98.2	970	5	PCT-US95-04681-11
5	4993.5	96.3	995	1	US-08-162-809-18
6	4971.5	95.8	1011	1	US-08-162-809-12
7	4962.5	95.7	995	2	US-08-673-789-5
8	3929.5	75.7	984	2	US-08-673-789-6
9	3723.5	71.8	951	1	US-08-162-809-2
10	3669	70.7	973	1	US-08-162-809-10
11	3662.5	70.6	988	1	US-08-162-809-14
12	3661.5	70.6	998	2	US-08-449-645A-20
13	3661.5	70.6	998	2	US-08-702-367A-20
14	3661.5	70.6	998	2	PCT-US95-04681-20
15	3608.5	69.6	970	2	US-08-673-789-7
16	3603.5	69.5	993	1	US-08-348-143-1
17	3603.5	69.5	993	1	US-08-571-785-1
18	3603.5	69.5	993	3	US-09-192-435-1
19	3603.5	69.5	993	4	US-08-558-340-1
20	3339.5	64.4	973	1	US-08-162-809-8
21	3053	58.8	991	2	US-08-449-645A-13
22	3053	58.8	991	2	US-08-702-367A-13
23	3053	58.8	991	5	PCT-US95-04681-13
24	3049	58.8	967	2	US-08-449-645A-30
25	3049	58.8	967	2	US-08-702-367A-30
26	3048	58.8	953	4	US-09-751-389-7
27	3046	58.7	986	2	US-08-673-789-3

28	3045	58.7	986	2	US-08-449-645A-15
29	3045	58.7	986	2	US-08-702-367A-15
30	3045	58.7	986	5	PCT-US95-04681-15
31	3038	58.6	1104	1	US-08-222-616-36
32	3038	58.6	1104	3	US-08-446-648-36
33	3038	58.6	1104	4	US-09-982-610-36
34	3038	58.6	1104	5	PCT-US95-04228-36
35	3031	58.4	975	4	US-09-751-389-8
36	3028	58.4	998	2	US-08-449-645A-17
37	3028	58.4	998	2	US-08-702-367A-17
38	3028	58.4	998	5	PCT-US95-04681-17
39	3020.5	58.2	993	3	US-08-368-776A-11
40	3013	58.1	998	3	US-08-368-776A-2
41	3013	58.1	998	5	PCT-US96-00419-2
42	3003	57.9	994	3	US-08-368-776A-12
43	2928	56.4	968	4	US-09-751-389-6
44	2927	56.4	983	1	US-08-162-809-16
45	2926	56.4	1005	2	US-08-469-537A-103
46	2924.5	56.4	983	2	US-08-449-645A-21
47	2924.5	56.4	983	2	US-08-702-367A-21
48	2924.5	56.4	983	5	PCT-US95-04681-21
49	2921.5	56.3	983	1	US-08-167-919A-10
50	2921.5	56.3	983	3	US-08-715-106-10
51	2921.5	56.3	983	4	US-09-442-649-10
52	2915.5	56.2	982	2	US-08-673-789-4
53	2844	54.8	987	1	US-08-436-044-6
54	2844	54.8	987	2	US-08-436-054-6
55	2844	54.8	987	5	PCT-US95-08813-6
56	2844	54.8	1276	3	US-08-222-616-24
57	2844	54.8	1276	3	US-08-446-648-24
58	2844	54.8	1276	4	US-09-982-610-24
59	2844	54.8	1276	5	PCT-US95-04228-24
60	2829	54.5	1036	4	US-09-751-389-2
61	2809.5	54.2	1035	4	US-09-751-389-4
62	2728.5	52.6	849	1	US-08-162-809-6
63	2726.5	52.6	849	2	US-08-673-789-10
64	2633.5	50.8	928	1	US-08-442-248-2
65	2633.5	50.8	928	1	US-08-440-815-2
66	2633.5	50.8	928	3	US-08-486-449-2
67	2633.5	50.8	928	4	US-08-578-684-2
68	2599.5	50.1	948	2	US-08-469-537A-101
69	2599.5	50.1	948	4	US-09-751-389-5
70	2464	47.5	877	2	US-08-673-789-2
71	2356.5	45.4	976	2	US-08-449-645A-18
72	2356.5	45.4	976	2	US-08-702-367A-18
73	2356.5	45.4	976	5	PCT-US95-04681-18
74	2347	45.2	977	2	US-08-673-789-8
75	2271	43.8	722	1	US-08-162-809-4
76	2271	43.4	744	1	US-08-162-809-20
77	2243	43.2	612	2	US-08-673-789-11
78	2179	42.0	710	1	US-08-162-809-22
79	2156.5	41.6	942	4	US-10-004-542-2
80	2156.5	41.6	942	4	US-10-430-797-2
81	2010	38.7	687	2	US-08-449-645A-29
82	2010	38.7	687	2	US-08-702-367A-29
83	1850.5	35.7	984	2	US-08-449-645A-19
84	1850.5	35.7	984	2	US-08-702-367A-19
85	1850.5	35.7	984	5	PCT-US95-04681-19
86	1847.5	35.6	984	2	US-08-673-789-9
87	1549	29.9	490	2	US-08-673-789-13
88	1475	28.4	610	3	US-08-368-776A-3
89	1475	28.4	610	5	PCT-US96-00419-3
90	1472.5	28.4	626	3	US-08-368-776A-5
91	1472.5	28.4	626	5	PCT-US96-00419-5
92	1181.5	22.8	371	2	US-08-673-789-14
93	953.5	18.4	307	4	US-09-270-767-45659
94	860.5	16.6	279	2	US-08-701-191A-23
95	860.5	16.6	279	4	US-09-664-526-23
96	784.5	15.1	265	3	US-09-799-345-4
97	784.5	15.1	265	3	US-09-962-276-4
98	783.5	15.1	265	3	US-09-799-345-5
99	783.5	15.1	265	3	US-09-799-345-6
100	783.5	15.1	265	4	US-09-962-276-5

Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 36, Appl  
Sequence 36, Appl  
Sequence 36, Appl  
Sequence 36, Appl  
Sequence 8, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 11, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 12, Appl  
Sequence 6, Appl  
Sequence 16, Appl  
Sequence 103, Appl  
Sequence 21, Appl  
Sequence 21, Appl  
Sequence 21, Appl  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 10, Appl  
Sequence 4, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 24, Appl  
Sequence 24, Appl  
Sequence 24, Appl  
Sequence 24, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 101, Appl  
Sequence 5, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 20, Appl  
Sequence 11, Appl  
Sequence 22, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 29, Appl  
Sequence 29, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 9, Appl  
Sequence 13, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 14, Appl  
Sequence 45659, A  
Sequence 23, Appl  
Sequence 23, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 5, Appl  
Sequence 5, Appl

## ALIGNMENTS

## RESULT 1

US-08-542-635-2  
 ; Sequence 2, Application US/08542635  
 ; Patent No. 6218356  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pawson, Anthony  
 ; APPLICANT: Henkemeyer, Mark  
 ; APPLICANT: Letwin, Kenneth  
 ; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR  
 ; TITLE OF INVENTION: TYROSINE KINASE  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Bereskin & Parr  
 ; STREET: 40 King Street West, Box 401  
 ; CITY: Toronto  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: M5H 3Y2  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/542,635  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McDiarmid, Shona S.  
 ; REGISTRATION NUMBER: 38,798  
 ; REFERENCE/DOCKET NUMBER: 3153-162  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (416) 364-7311  
 ; TELEFAX: (416) 361-1398  
 ; TELEX: 06-23115  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 994 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Mus musculus  
 ; DEVELOPMENTAL STAGE: Embryo  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: lamda gt10 cDNA library  
 ; CLONE: Combined pNURACE A2 and K2 and cDNA clones  
 ; POSITION IN GENOME:  
 ; CHROMOSOME/SEGMENT: Distal end of chromosome 4  
 ; MAP POSITION: near the ahd-1 mutation  
 ; US-08-542-635-2

Query Match 98.9%; Score 5130; DB 3; Length 994;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy	10	LLLLPLAAVEETLMDSTTATAELGWMVHPSPSGWEEVSGYDENNTTIRTYQVCNVFESSQ	69
Db	18	LLLLPLAAVEETLMDSTTATAELGWMVHPSPSGWEEVSGYDENNTTIRTYQVCNVFESSQ	77
Qy	70	NNWLRTKFIARRGAHRHIVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADFDSATKTFPN	129
Db	78	NNWLRTKFIARRGAHRHIVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADFDLATKTFPN	137
Qy	130	WMENPWKVDTIAADESFQVLDGRVWKINTEVRSFGPVSRSGFYLAFOYGGCMSLIA	189
Db	138	WMENPWKVDTIAADESFQVLDGRVWKINTEVRSFGPVSRNGFYLAFOYGGCMSLIA	197

Qy	190	VRVYRKCPRIIONGAIFOETLSGAESTSLVAARGSCIANAEBVDVPIKLYCNGDGEWLV	249
Db	198	VRVYRKCPRIIONGAIFOETLSGAESTSLVAARGSCIANAEBVDVPIKLYCNGDGEWLV	257
Qy	250	PIGRCKAGFEAVENGTVCRGCPSTFKANQDEACTHCPINSRTTSEGATNCVCRNGY	309
Db	258	PIGRCKAGFEAVENGTVCRGCPSTFKANQDEACTHCPINSRTTSEGATNCVCRNGY	317
Qy	310	YRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSCGREDLVNIIICKSCGSGR	369
Db	318	YRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSCGREDLVNIIICKSCGSGR	377
Qy	370	GACTRCGDNVQYAPROGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPFSQFASVNI	429
Db	378	GACTRCGDNVQYAPROGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPFSQFASVNI	437
Qy	430	TINQAAPSASVIMHQVSRVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSP	489
Db	438	TINQAAPSASVIMHQVSRVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSP	497
Qy	490	TNTVTVOGLKAGAIYVQVRAVAGYGRYSGKMYFQTMTEAEVQTSIOEKLPLIGSSA	549
Db	498	TNTVTVOGLKAGAIYVQVRAVAGYGRYSGKMYFQTMTEAEVQTSIOEKLPLIGSSA	557
Qy	550	AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDNEAV	609
Db	558	AGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDNEAV	617
Qy	610	REFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFLS	669
Db	618	REFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFLS	677
Qy	670	EASIMQOFDHPNVIHLEGVVTKSTPMIITEFMENGLSDSLFRQNDQOFTVIOLVGMRLG	729
Db	678	EASIMQOFDHPNVIHLEGVVTKSTPMIITEFMENGLSDSLFRQNDQOFTVIOLVGMRLG	737
Qy	730	IAAGMKYLADNMVYVHRDLAARNILVNSNLVCKVSDFLSRFLEDDTSDPTTYSALGKIP	789
Db	738	IAAGMKYLADNMVYVHRDLAARNILVNSNLVCKVSDFLSRFLEDDTSDPTTYSALGKIP	797
Qy	790	IRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYDMTNDQVINAIQDYRLPPPM	849
Db	798	IRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYDMTNDQVINAIQDYRLPPPM	857
Qy	850	DCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSGINPLLDRTI	909
Db	858	DCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSGINPLLDRTI	917
Qy	910	PDYTSFNTVDEWLEAIKMGQYKESFANAGTSPDVSQMMEDILRLGVTLAGHQKILN	969
Db	918	PDYTSFNTVDEWLEAIKMGQYKESFANAGTSPDVSQMMEDILRLGVTLAGHQKILN	977
Qy	970	SIQWMRAQMNQIOSVEV 986	
Db	978	SIQWMRAQMNQIOSVEV 994	

## RESULT 2

US-08-449-645A-11  
 ; Sequence 11, Application US/08449645A  
 ; Patent No. 5981245  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fox, Gary M.  
 ; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
 ; TITLE OF INVENTION: Kinases  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Amgen Patent Operations/RBW  
 ; STREET: 1840 Dehavilland Drive  
 ; CITY: Thousand Oaks  
 ; STATE: California  
 ; COUNTRY: USA



Qy	195	RKCPRIIQNGAIFQETLGSABSTSLVAARGSCIANAEVDPVKLYCNGDGEWLVPIGR	254
Db	181	RKCPRIIQNGAIFQETLGSABSTSLVAARGSCIANAEVDPVKLYCNGDGEWLVPIGR	240
Qy	255	MCKAGFEAVENGTVCRGCPSGTFFKANQDEACTHCPINSRTTSEGATNCVCRNGYRADL	314
Db	241	MCKAGFEAVENGTVCRGCPSGTFFKANQDEACTHCPINSRTTSEGATNCVCRNGYRADL	300
Qy	315	DLPLMPCCTTIPSAQAVISSVNETSLMLEWTPPRDSSGREDLVNIIICKSCSGRGACTR	374
Db	301	DLPLMPCCTTIPSAQAVISSVNETSLMLEWTPPRDSSGREDLVNIIICKSCSGRGACTR	360
Qy	375	CGDNVOYAPROLGLTEPRIYISDLIAHTQYTFEIOAVNGVTDQSPSPQFASVNIITNOA	434
Db	361	CGDNVOYAPROLGLTEPRIYISDLIAHTQYTFEIOAVNGVTDQSPSPQFASVNIITNOA	420
Qy	435	APSAVIMHOVSRVDSITLSWSQDPQNGVILDEYLOYYEKELSEYNATAIKSPNTVT	494
Db	421	APSAVIMHOVSRVDSITLSWSQDPQNGVILDEYLOYYEKELSEYNATAIKSPNTVT	480
Qy	495	VQGLKAGAIYVQVQVARTVAGVGRYSGKWYFQTMTEAEYQTSIOEKLPLIIGSSAAGLV	554
Db	481	--GLKAGAIYVQVQVARTVAGVGRYSGKWYFQTMTEAEYQTSIOEKLPLIIGSSAAGLV	538
Qy	555	LIAVVVIAIVCNRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPFTYEDPNEAVREFAK	614
Db	539	LIAVVVIAIVCNRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPFTYEDPNEAVREFAK	598
Qy	615	EIDISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVALKTLKSGYTEKQRDRDPLSEASIM	674
Db	599	EIDISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVALKTLKSGYTEKQRDRDPLSEASIM	658
Qy	675	GQFDHPNVIHLEGVTKSTPVMIIIFPMENGSLDSFLQRNDGQFTVIQLVGMRLGIAAGM	734
Db	659	GQFDHPNVIHLEGVTKSTPVMIIIFPMENGSLDSFLQRNDGQFTVIQLVGMRLGIAAGM	718
Qy	735	KYLADNMVYHRDLAARNILVNSLCKYSDPGLSRFLEDDTSDPTYSALGGKIPIRWTA	794
Db	719	KYLADNMVYHRDLAARNILVNSLCKYSDPGLSRFLEDDTSDPTYSALGGKIPIRWTA	778
Qy	795	PEAIQYRKFTSASDVMSYGIYVWMEVMSYGERPYWDMTNOQVINAIEQDYRLPPMDCPSA	854
Db	779	PEAIQYRKFTSASDVMSYGIYVWMEVMSYGERPYWDMTNOQVINAIEQDYRLPPMDCPSA	838
Qy	855	LHQMLDCWQKORNRHPKFGQIVNTLDMIRNPNSLKAWAPLSSGINLPLLDRTIPDYS	914
Db	839	LHQMLDCWQKORNRHPKFGQIVNTLDMIRNPNSLKAWAPLSSGINLPLLDRTIPDYS	898
Qy	915	FNTVDEWLEAIKWQYKESFANAGFTSFDVWSOMMEDILRLGVTLAGHQKKILNSIQVM	974
Db	899	FNTVDEWLEAIKWQYKESFANAGFTSFDVWSOMMEDILRLGVTLAGHQKKILNSIQVM	958
Qy	975	RAQMNQIQSVEV 986	
Db	959	RAQMNQIQSVEV 970	

481	DB	--GLKAGAIYVQVRARFTVAGYGRYSKGMVFQWMEABYQ'ISIQEKUPLILGSSAAGUJVF	336
555	QY	LIAVVVTAIACNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTFYEDPNEAVREFAK	614
539	DB	LIAVVVTAIACNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTFYEDPNEAVREFAK	598
615	QY	EIDISCVKIEQIVGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFLSEASIM	674
599	DB	EIDISCVKIEQIVGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFLSEASIM	658
675	QY	GQDHPNVIHLEGVVTKSTPMWIIETPEWNGSLDSFLRQNDGQFTVQLVGMRLGIAAGM	734
659	DB	GQDHPNVIHLEGVVTKSTPMWIIETPEWNGSLDSFLRQNDGQFTVQLVGMRLGIAAGM	718
735	QY	KYLADMYVHRDLAARNILVNSNLVKCVSDFGLSRFLEDDTSDPTYSALGGKPIRWTA	794

```

RESULT 4
PCT-US95-04681-11
; Sequence 11, Application PC/TUS9504681
;
; GENERAL INFORMATION:
;
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
;

```

Db 719 KYLDAMNVRHDLAARNILVNSLVKVSDFGLSRFLEDDTSDPTTYSALGKGKPIRMTA 778  
Qy 795 PEALQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAIEQDYRLPPMDCPSA 854  
Db 779 PEALQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAIEQDYRLPPMDCPSA 838  
Qy 855 LHQLMLDCWKQDRNHRPKFGQIVNTLDMIRNPNLSLKAMAPLSSGINLPLDRTIPDYS 914  
Db 839 LHQLMLDCWKQDRNHRPKFGQIVNTLDMIRNPNLSLKAMAPLSSGINLPLDRTIPDYS 898  
Qy 915 FNTVDEWLEAIKMGQYKESFANAGFTSDVVVSQMMEDILRLGVTLAGHOKKILNSTQVM 974  
Db 899 FNTVDEWLEAIKMGQYKESFANAGFTSDVVVSQMMEDILRLGVTLAGHOKKILNSTQVM 958  
Qy 975 RAQNMNQISQVEV 986  
Db 959 RAQNMNQISQVEV 970

RESULT 5  
US-08-162-809-18  
; Sequence 18, Application US/08162809  
; Patent No. 5457048  
; GENERAL INFORMATION:  
; APPLICANT: Pasquale, Elena B.  
; APPLICANT: Sajjadi, Fereydoun G.  
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/162,809  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 9503  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 995 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-162-809-18

Query Match 96.3%; Score 4993.5; DB 1; Length 995;  
Best Local Similarity 95.8%; Pred. No. 0;  
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;

Qy 10 LLLPLAAVEETLMDSTTATAELGWMVHPSPSGHEEYSGYDENNMNTTIRTYQVCNVPESQ 69  
Db 18 LALLPLAAVEETLMDSTTATAELGWMVHPSPSGHEEYSGYDENNMNTTIRTYQVCNVPESQ 77  
Qy 70 NNWLRTKPIRRGAHRHIVEMKFSVRDCSSIPSPGSKCTFNLYYYEADPDSATKTFPN 129  
Db 78 NNWLRTKPIRRGAHRHIVEMKFSVRDCSSIPNVPGSKCTFNLYYYESDFDSATKTFPN 137  
Qy 130 WMENPMVKVDITAADESFQVDLGGVRVWKINTEVRSGFVSRSGFYLAQDYGCGMSLIA 189

Db 138 WMENPMVKVDITAADESFQVDLGGVRVWKINTEVRSGFVSRSGFYLAQDYGCGMSLIA 197  
Qy 190 VRVYRKCPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGWLV 249  
Db 198 VRVYRKCPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGWLV 257  
Qy 250 PIGRCMKAGFEAVENGTCVRCGCPSTGTFKANOQDEACTHCPINSRTTSEGNATNCVCRNGY 309  
Db 258 PIGRCMKAGFEAVENGTCVRCGCPSTGTFKANOQDEACTHCPINSRTTSEGNATNCVCRNGY 317  
Qy 310 YRADLDPLMPCPTTIPSAQAVISSVNETSLMELWTPPRSGGREDLVYNIICKSCSGR 369  
Db 318 YRADADPVDMPCTTIPSAQAVISSVNETSLMELWTPPRSGGREDLVYNIICKSCSGR 377  
Qy 370 GACTRCGDNVQAPROLGLTEPRIYISDLAHTQYTFEIOAVNGVTPQSPPOFASVNI 429  
Db 378 GACTRCGDNVQAPROLGLTEPRIYISDLAHTQYTFEIOAVNGVTPQSPPOFASVNI 437  
Qy 430 TTNQAAFSAVSIMHQVSRTVDSITLSMSQDPQPNQVILDYELQYKEKSELYNATAIKSP 489  
Db 438 TTNQAAFSAVSIMHQVSRTVDSITLSMSQDPQPNQVILDYELQYKEKSELYNATAIKSP 497  
Qy 490 TINTVVOGLKAGAIYVQVRAARTVAGYGRYSGRMVYFOTMTEAEYQTSIOEKLPLIIGSSA 549  
Db 498 TINTVVOGLKAGAIYVQVRAARTVAGYGRYSGRMVYFOTMTEAEYQTSIOEKLPLIIGSSA 557  
Qy 550 AGLVELIAVVVIAVCN-REGFERADSEYDQKQHTYSGHMTGCMKIYIDPFTVEDPNEA 608  
Db 558 AGLVELIAVVVIAVCN-REGFERADSEYDQKQHTYSGHMTGCMKIYIDPFTVEDPNEA 617  
Qy 609 VREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDRDL 668  
Db 618 VREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDRDL 677  
Qy 669 SEASIMQFDPHNVHLEGVVTGKSTPVMITTEPMENGLSDSFLRQNDGQFTVIQVGLMR 728  
Db 678 SEASIMQFDPHNVHLEGVVTGKSTPVMITTEPMENGLSDSFLRQNDGQFTVIQVGLMR 737  
Qy 729 GIAAGMKYLDAMNVRHDLAARNILVNSLVKVSDFGLSRFLEDDTSDPTTYSALGKGK 788  
Db 738 GIAAGMKYLDAMNVRHDLAARNILVNSLVKVSDFGLSRFLEDDTSDPTTYSALGKGK 797  
Qy 789 PIRWTAPEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAIEQDYRLPPP 848  
Db 798 PIRWTAPEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAIEQDYRLPPP 857  
Qy 849 MDCPSALHQLMLDCWKQDRNHRPKFGQIVNTLDMIRNPNLSLKAMAPLSSGINLPLDRT 908  
Db 858 MDCPSALHQLMLDCWKQDRNHRPKFGQIVNTLDMIRNPNLSLKAMAPLSSGINLPLDRT 917  
Qy 909 IPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSDVVVSQMMEDILRLGVTLAGHOKKIL 968  
Db 918 IPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSDVVVSQMMEDILRLGVTLAGHOKKIL 977  
Qy 969 NSIQVMRAQNMNQISQVEV 986  
Db 978 NSIQVMRAQNMNQISQVEV 995

RESULT 6  
US-08-162-809-12  
; Sequence 12, Application US/08162809  
; Patent No. 5457048  
; GENERAL INFORMATION:  
; APPLICANT: Pasquale, Elena B.  
; APPLICANT: Sajjadi, Fereydoun G.  
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 La Jolla Village Drive, Suite 700

618	Db	MKVIDPFTYEDPNEAVREFAKEIDISCVKIBQVIGAFGEVCSGHUKLPKKEIFVAL	677
653	Qy	KTLKSGYTEKORRDFLSEASIMQGDHPHNVHLEGVVTKSPVMIITFEMENGSLDSFLR	712
678	Db	KTLKSGYTEKORRDFLSEASIMQGDHPHNVHLEGVVTKSPVMIITFEMENGSLDSFLR	737
713	Qy	QNDGQFTVIOVLQVGLRGIAAGMKYIADMYVHRDIAARNILVNSLVCKVSDFGLSRPLE	772
738	Db	QNDGQFTVIOVLQVGLRGIAAGMKYIADMYVHRDIAARNILVNSLVCKVSDFGLSRPLE	797
773	Qy	DDTSDPFTYSALGCKPIRWTAPRAIOYRKFTSASDVMSYGIVMVMSYGERPYWDMTN	832
798	Db	DDTSDPFTYSALGCKPIRWTAPRAIOYRKFTSASDVMSYGIVMVMSYGERPYWDMTN	857
833	Qy	QDVINAIEQDYRLPPPPMDCPSALHQLMLDCWQKORNRHPKFGQIVNTLDDKMI RPNLSKA	892
858	Db	QDVINAIEQDYRLPPPPMDCPSALHQLMLDCWQKORNRHPKFGQIVNTLDDKMI RPNLSKA	917
893	Qy	MAPLSSGINPLLDRTIPDTSNTVDEWLEALKMGOYKESFANAGFTSFDFVVSOMMED	952
918	Db	MAPLSSGINPLLDRTIPDTSNTVDEWLEALKMGOYKESFANAGFTSFDFVVSOMMED	977
953	Qy	ILRUGVTLAGHOKKILNSIQVMEQAQMQIQSVEV	986
978	Db	ILRUGVTLAGHOKKILNSIQVMEQAQMQIQSVEV	1011
RESULT 7			
US-08-673-789-5			
; Sequence 5, Application US/08673789			
; Patent No. 5814479			
; GENERAL INFORMATION:			
; APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,			
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,			
; TITLE OF INVENTION: BSK RECEPTOR LIKE			
; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR			
; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC			
; NUMBER OF SEQUENCES: 14			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: MORGAN & FINNEGAN			
; STREET: 345 PARK AVENUE			
; CITY: NEW YORK			
; STATE: NEW YORK			
; COUNTRY: USA			
; ZIP: 10154			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: FLOPPY DISK			
; COMPUTER: IBM PC COMPATIBLE			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: WORDPERFECT 5.1			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/673,789			
; FILING DATE:			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/177,812			
; FILING DATE: 04-JAN-1994			
; ATTORNEY/AGENT INFORMATION:			
; NAME: CAROL M. GRUPPI			
; REGISTRATION NUMBER: 37,341			
; REFERENCE/DOCKET NUMBER: 2026-4105			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (212) 758-4800			
; TELEFAX: (212) 751-6849			
; TELEX: 421792			
; INFORMATION FOR SEQ ID NO: 5:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 995			
; TYPE: AMINO ACID			
; STRANDEDNESS: UNKNOWN			

TOPOLOGY: UNKNOWN  
US-08-673-789-5

Query Match 95.7%; Score 4962.5; DB 2; Length 995;  
Best Local Similarity 95.1%; Pred. No. 0;  
Matches 930; Conservative 30; Mismatches 17; Indels 1; Gaps 1;

Qy 10 LLLPLLAABEETLMDSTATAELGMMVHPSPGWEVSGYDENNMNTIRTYQCVNFESSQ 69  
Db 18 LALLPLLAABEETLMDSTATAELGMMVHPSPGWEVSGYDENNMNTIRTYQCVNFESSQ 77

Qy 70 NNWLRTKPIRRGAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSATKTPPN 129  
Db 78 NNWLRTKPIRRGAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSATKTPPN 137

Qy 130 WMENPWKVDITIAADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOYGGCMSLIA 189  
Db 138 WMENPWKVDITIAADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOYGGCMSLIA 197

Qy 190 VRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGWLV 249  
Db 198 VRVYRKCPRVIONGAVFQETLSGAESTSLVAARGTCISNAEVDVPIKLYCNGAGWLV 257

Qy 250 PIGRCMKAGFEAVENGTVCKGSPGTFKANOQDEACTHCPIINSTRTTSEGNATNCVCRNGY 309  
Db 258 PIGRCMCRPGYESVENGTVCKGSPGTFKASQSGDEGCVHCPINSTRTTSEGNATNCVCRNGY 317

Qy 310 YRADLPDLPDCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCGSR 369  
Db 318 YRADADPVDMPCTTIPAPQAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCGSR 377

Qy 370 GACTRCGDNQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTPQSPFOPASVNI 429  
Db 378 GACTRCGDNQYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTPQSPFOPASVNI 437

Qy 430 TTNOAAPSASIMHQVSRVDSITLSWSQDPQNGVILDVYELQYKELSEYNATAKSP 489  
Db 438 TTNOAAPSASIMHQVSRVDSITLSWSQDPQNGVILDVYELQYKELSEYNATAKSP 497

Qy 490 TMTVVOGLKAGALYVQVARTVAGYGRYSGKMFQMTAEAYQTSIOEKLPIIGSSA 549  
Db 498 TMTVVOQLKAGTIIYVQVARTVAGYGRYSGKMFQMTAEAYQTSVQSKLPIIIGSSA 557

Qy 550 AGLVFLIAVVIAIVCN-RRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDNEA 608  
Db 558 AGLVFLIAVVIIIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDNEA 617

Qy 609 VREFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQRDRL 668  
Db 618 VREFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKQRDRL 677

Qy 669 SEASIMQFHPNVIIHLEGVVTKTPVMIITEFMENGLSDSFLRNDQGFVIOLVGMRL 728  
Db 678 SEASIMQFHPNVIIHLEGVVTKTPVMIITEFMENGLSDSFLRNDQGFVIOLVGMRL 737

Qy 729 GIAAGMYLADMYVHRDLAARNILVNSLVCKYSDFGLSRFLDDTSDPTYSALGKI 788  
Db 738 GIAAGMYLADMYVHRDLAARNILVNSLVCKYSDFGLSRFLDDTSDPTYSALGKI 797

Qy 789 PIRWTAPEAIQYRKFTSASDVMSYGIIVWVEVMSYGERPYMDMTNQDVINAIEQDYRLPPP 848  
Db 798 PIRWTAPEAIQYRKFTSASDVMSYGIIVWVEVMSYGERPYMDMTNQDVINAIEQDYRLPPP 857

Qy 849 MDCPSALHOLMDCWQKDRNRPFGQIVNTLDXMIIRNPSLKAMAPLSSGINPLDRT 908  
Db 858 MDCPSALHOLMDCWQKDRNRPFGQIVNTLDXMIIRNPSLKAMAPLSSGINPLDRT 917

Qy 909 IPDYTSFNTVDEWLEAKMGQYKESFANAGFTSDVVSQMMEDILRLGVTLAGHQKIL 968  
Db 918 IPDYTSFNTVDEWLEAKMGQYKESFANAGFTSDVVSQMMEDILRLGVTLAGHQKIL 977

Qy 969 NSIQVMRAQMNQIQSVEV 986  
|||||

Db 978 NSIQVMRAQMNQIQSVEV 995

## RESULT 8

US-08-673-789-6  
; Sequence 6, Application US/08673789  
; Patent No. 5814479  
; GENERAL INFORMATION:

APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,  
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,  
APPLICANT: GEORGE, F.  
TITLE OF INVENTION: BSK RECEPTOR LIKE  
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR  
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC  
TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA: US/08/673,789  
APPLICATION NUMBER: US/08/673,789  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA: 08/177,812  
APPLICATION NUMBER: 04-JAN-1994  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4105  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 984  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
US-08-673-789-6

Query Match 75.7%; Score 3929.5; DB 2; Length 984;  
Best Local Similarity 73.8%; Pred. No. 9e-284;  
Matches 719; Conservative 128; Mismatches 126; Indels 1; Gaps 1;

Qy 11 LLLPLLAABEETLMDSTATAELGMMVHPSPGWEVSGYDENNMNTIRTYQCVNFESSQ 70

Db 10 LLASAVAAMEETLMDSETATAEIGWTANPASGWEVSGYDENLNTIRTYQCVNFEPNQ 69

Qy 71 NWLRTKPIRRGAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSATKTPPN 130

Db 70 NWLRTKPIRRGAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSATKTPPN 129

Qy 131 MENPWKVDITIAADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOYGGCMSLIAV 190

Db 130 SEAPYLKVDITIAADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOYGGCMSLIAV 189

Qy 191 RVFVRCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGWLV 250

Db 190 RVFVRCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGWLV 249

Qy 251 IGRCMKAGFEAVENGTVCKGSPGTFKANOQDEACTHCPIINSTRTTSEGNATNCVCRNGY 310

|||||

Db 250 IGRCTKAGYEP-ENSVACKACAPAGTFKASQAEAGCSHCPSNSRSPSEASPICTCTGYY 308  
QY 311 RADLDPLDMPCTTTPSAQAVISVNETSLMLETTPRDSGREDLVNLIICKSGSGRG 370  
Db 309 RADDPPEVACTSPVSGRNNVISVNETSILLEWHPPRETGRDDVTYNIICKRCADDR 368  
QY 371 ACTRCGNVOYAPQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQASVNIT 430  
Db 369 SCSCDDNVEVPQLGLTECRVSISSLWHTPTFDIQAINGVSSKSPFPPOHVSNIT 428  
QY 431 TNOAPSASVIMHOVSRVTSITLSWSQDPQNGVILDYELQYKEKELSEYNATAKSPT 490  
Db 429 TNOAAPSTVPMHQSATMSITLSWQPEQNGIILDIYRIYKEHNEFNSMARST 488  
QY 491 NTVTVOGLKAGIYVFOVARTVAGYGRYSKMYFQTMTEAEXOTSIOEKLPLIGSSAA 550  
Db 489 NTARIDGLRPMGVYVQVARTVAGYGRYSKMYFQTMTEAEXOTSIOEKLPLIGSSAA 548  
QY 551 GLVELIAVWIAIYCNRRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPFTYEDNEAVR 610  
Db 549 GVVPVSVLVAISVCSKRAYSKEAVYSDKLQHYSTGRGSPGMKIYIDPFTYEDNEAVR 608  
QY 611 EFAKEIDISCKIBQVTCAGFGEVCSGHLKLPKREIYVAIKTLKSGYTEKQRDPFSE 670  
Db 609 EFAKEIDVSFKIBEVTCAGFGEVCSGHLKLPKREIYVAIKTLKAGYSEKQRDPFSE 668  
QY 671 ASIMGQDHPNVIHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVIQVGMURGI 730  
Db 669 ASIMGQDHPNVIHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVIQVGMURGI 728  
QY 731 AAGMKYLADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYSALGGKIP 790  
Db 729 AAGMKYLADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYSALGGKIP 788  
QY 791 RWTAPAIQVTKFTSASDVMSYGYIMVEMVSYGIRPYWDMTNQDVINAISQDYLPPMD 850  
Db 789 RWTAPAIQVTKFTSASDVMSYGYIMVEMVSYGIRPYWDMTNQDVINAISQDYLPPMD 848  
QY 851 CPSALHQLMDCWOKDRNRPKFGQIVNTLDKMRNPSLKMAMPLSSGILNPLDRTIP 910  
Db 849 CPAALHQLMDCWOKDRNRPKFGQIVNTLDKMRNPSLKMAMPLSSGILNPLDRTIP 908  
QY 911 DYTSTNTVDLEAIKMGQYKESFANAGTSPFVVSQMMEDILRLGVTLAGHQKILNS 970  
Db 909 DFTAFTVDDWLSAIVMVOYRDSPLTGTSLQVLTQWTSDDLRIQVTLAGHQKILNS 968  
QY 971 IQVRAQWQIQSV 984  
Db 969 IHSMRVQWQNSPSV 982

RESULT 9  
US-08-162-809-2  
; Sequence 2, Application US/08162809  
; Patent No. 5457048  
; GENERAL INFORMATION:  
; APPLICANT: Pasquale, Elena B.  
; APPLICANT: Sajjadi, Pereyoudun G.  
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego,  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/162,809  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 9503  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 951 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-162-809-2

Query Match 71.8%; Score 3723.5; DB 1; Length 951;  
Best Local Similarity 70.3%; Pred. No. 1.9e-268;  
Matches 688; Conservative 121; Mismatches 117; Indels 53; Gaps 3;  
QY 21 ETLMDSSTATAELGMMVHPSPSGWEEVSGYDENNTIRTYQVCNVFSSQNNWLRTKPIRR 80  
Db 1 ETLMDSSTATAELGMMVHPSPSGWEEVSGYDENNTIRTYQVCNVFSSQNNWLRTKPIRR 60  
QY 81 RGARHIVEMKFSVROCSSIPSPGCKETFNLYVEADPDSATKTFPNWMEVWVKVD 140  
Db 61 RGARHIVEMKFSVROCSSIPSPGCKETFNLYVEADPDSATKTFPNWMEVWVKVD 120  
QY 141 IAADESFSQVDLGRVWKNITEVRSFGPVSRSFYLAQDYGGCMSLIAVRVFRKCPRI 200  
Db 121 IAADESFSQVDLGRVWKNITEVRSFGPVSRSFYLAQDYGGCMSLIAVRVFRKCPRI 147  
QY 201 IQNGAIFQETLSAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRMCVAGF 260  
Db 148 VQNFAPFETMTAESTSLVARTGTCTPNAEEVDVPIKLYCNGDGEWLVPIGRMCVAGF 207  
QY 261 EAVENGTCVRCGPGTGFKAQNGDEACTHCPIINSRTTSEGATNCVCRNGYVRADLDPLDMP 320  
Db 208 EP-ENNVACRACFAGTGFKAQNGDEACTHCPIINSRTTSEGATNCVCRNGYVRADLDPLDMP 266  
QY 321 CTTIPSAQAVISVNETSILMLETTPRDSGREDLVNLIICKSGSGRGAACRCGDNVQ 380  
Db 267 CTSVPSPGRNVISVNETSILMLETTPRDSGREDLVNLIICKSGSGRGAACRCGDNVQ 326  
QY 381 YAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQASVNITNQAAPSAVS 440  
Db 327 FVPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQASVNITNQAAPSAVS 386  
QY 441 IMHOVSRVTSITLSWSQDPQNGVILDYELQYKEKELSEYNATAKSPT 481  
Db 387 IMHOVSRVTSITLSWSQDPQNGVILDYELQYKEKELSEYNATAKSPT 446  
QY 482 NATAIKSPNTVTVOGLKAGIYVFOVARTVAGYGRYSKMYFQTMTEAEXOTSIOEKL 541  
Db 447 NSSVARSQNTNARLEGLRPMGVYVQVARTVAGYGRYSKMYFQTMTEAEXOTSIOEKL 506  
QY 542 PLIIGSAAAGLVFLIAVWIAIYCNRRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPFT 601  
Db 507 PLIIGSAAAGLVFLIAVWIAIYCNRRGFERADSEYTDKLOHYTSGHMTFGMKIYIDPFT 566  
QY 602 YEDPNEAVREFAKEIDISCKIBQVTCAGFGEVCSGHLKLPKREIYVAIKTLKAGYSE 661  
Db 567 YEDPNEAVREFAKEIDISCKIBQVTCAGFGEVCSGHLKLPKREIYVAIKTLKAGYSE 626  
QY 662 KORRDFLSEASIMGQDHPNVIHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVI 721  
Db 627 KORRDFLSEASIMGQDHPNVIHLEGVVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVI 686  
QY 722 QLVGMRLGIAAGMKYLADNMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYS 781



Db 687 QLVGMLRGIAAGMKYLAEMNNVYHRLDLAARNILVNSNLVCKYDFGLSRYLQDDTSDPTT 746  
Qy 782 SALGKPIRWTAPETAIQYRKFTSASDVWSYGIWVWVMSYGERPYWDMTQDVINAIEQ 841  
Db 747 SSLGKPIRWTAPETAIQYRKFTSASDVWSYGIWVWVMSYGERPYWDMTQDVINAIEQ 806  
Qy 842 DYRLPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGIN 901  
Db 807 DYRLPPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGIN 866  
Qy 902 LPLDRTIPDVTSTNTVDWELAIKMGYKESFANAGTSDVVSQMMEDILBLGVTLA 961  
Db 867 QPLDRTIPDVTSTNTVDWELAIKMGYKESFANAGTSDVVSQMMEDILBLGVTLA 926  
Qy 962 GHQKKILNSIQVMAQMNQ 980  
Db 927 GHQKKILNSIQVMAQMNQ 945

RESULT 10  
US-08-162-809-10  
; Sequence 10, Application US/08162809  
; Patent No. 5457048  
; GENERAL INFORMATION:  
; APPLICANT: Pasquale, Elena B.  
; APPLICANT: Sajjadi, Fereydoun G.  
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/162,809  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 9503  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 973 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-162-809-10

Query Match 70.7%; Score 3669; DB 1; Length 973;  
Best Local Similarity 71.1%; Pred. No. 2.2e-264;  
Matches 683; Conservative 121; Mismatches 145; Indels 12; Gaps 4;  
Qy 30 TAEIGWVHPSPGHEEVSVDENNTTQVNVFESSQNNWLRTPFRRGHRHVE 89  
Db 21 TSELAWTHPETGEEVSGYDEANNTTQVNVFESSQNNWLRTPFRRGHRHVE 80  
Qy 90 MKFSVRDCSSIPVSGCKETFNLYYEADPDSATKTFNNMNPWVKVDTIAADESFSQ 149  
Db 81 LKFTVDCNSIPNIPGSCETFNLYYEADPDSATKTFNNMNPWVKVDTIAADESFSK 140  
Qy 150 VDLGGVWKINTEVRSFGPVSRSFGYLAFOQDYGCCMSLIAVRFYRKCPRIIQNGAIFQE 209

Db 141 LESG----RVNTKVRSPGLSKNGFYLAFOQDYGCCMSLIAVRFYRKCPRIIQNGAIFQE 196  
Qy 210 TLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGCMCKAGFEAVENGTV 269  
Db 197 TLTGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGCMCKAGFEAVENGTV 256  
Qy 270 RGCPSTGTFKANQGDDEACTHCPINSRTTSEGATNCVCRNGYVRADLDPLDMCTTIPSAPO 329  
Db 257 QACGPGTFKSKQGEPCSPCPNSRTTGAATVCIHSGFFRADADPADSACTSVPSAPR 316  
Qy 330 AVTSVNETSLMLEWTTPRDSGREDLVYNIICKSCGSGRACATCGDNTVOYARQL--- 386  
Db 317 SVISVNETSLMLEWTTPRDSGREDLVYNIICKSCGSGRACATCGDNTVOYARQL--- 376  
Qy 387 GLTEPRIYISDLAHTOYTFEIOAVNGVTDQSPSPQFASVNIITNQAAPSIVMHOVS 446  
Db 377 GLTERRIYISKWAHPQITFEIOAVNGVTDQSPSPQFASVNIITNQAAPSIVMHOVS 436  
Qy 447 RTVDSITLSWSQDPQNGVILDYELQYKE-LSEYNATAIKSPNTVTVOGLKAGAIYV 505  
Db 437 STGNSMTLSWTPPERPNIILDYELQYKE-LSEYNATAIKSPNTVTVOGLKAGAIYV 496  
Qy 506 FQVRAATVAGYGRYSGMYFQMTAEAYQTSIOEKLPLIIGSSAAGLVFLIIVVIAIVC 565  
Db 497 VQVRAATVAGYGRYSLPTEFTTAEDGSTSKTQELPLIVGSATAGLFLVIVVIAIVC 556  
Qy 566 NRGFERADSEYTDKLOHTSGHMTGCMKIYIDPFTVEDPNEAREFAKEDIDISCVKIEQ 625  
Db 557 FRKORNSDPEYTEKQY---VTPGMKVYIDPFTVEDPNEAREFAKEDIDISCVKIEE 612  
Qy 626 VIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTERQRDRFLSEASIMQFDPNVIHL 685  
Db 613 VIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTERQRDRFLSEASIMQFDPNVIHL 672  
Qy 686 EGVVTKSRPVIITEFMENGLSFLRQNDQFTVIOLVGLRGIAAGMKYLAEMNNVYH 745  
Db 673 EGVVTKSRPVIITEFMENGLSFLRQNDQFTVIOLVGLRGIAAGMKYLAEMNNVYH 732  
Qy 746 DLAAARNILVNSNLVCKYDFGLSRYLQDDTSDPTT 792  
Db 733 DLAAARNILVNSNLVCKYDFGLSRYLQDDTSDPTT 792  
Qy 806 ASDVWSYGIWVWVMSYGERPYWDMTQDVINAIEQ 865  
Db 793 ASDVWSYGIWVWVMSYGERPYWDMTQDVINAIEQ 852  
Qy 866 DRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGIN 925  
Db 853 DRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSSGIN 912  
Qy 926 KMGYKESFANAGTSDVVSQMMEDILBLGVTLAGHOKKILNSIQVMAQMNQ 985  
Db 913 KMGYKESFANAGTSDVVSQMMEDILBLGVTLAGHOKKILNSIQVMAQMNQ 972  
Qy 986 V 986  
Db 973 V 973

RESULT 11  
US-08-162-809-14  
; Sequence 14, Application US/08162809  
; Patent No. 5457048  
; GENERAL INFORMATION:  
; APPLICANT: Pasquale, Elena B.  
; APPLICANT: Sajjadi, Fereydoun G.  
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 La Jolla Village Drive, Suite 700

```
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatenIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,809
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-162-809-14

Query Match 70.6%; Score 3662.5; DB 1; Length 998;
Best Local Similarity 70.1%; Pred. No. 6.9e-264;
Matches 684; Conservative 121; Mismatches 144; Indels 27; Gaps 5;

QY 30 TAEIGWVHPSPGVEEYSGYDENMNTIRTVQCVNFESSQNNMLRTKFIERRGGAHRHVE 89
DB 21 TSELATWTHETGVEEYSGYDEANPIRTVQCVNREANQNNMLRTKFIQDQVQRYVE 80
QY 90 MKFSVRDCSSIPSPGSKETFNLYEADPDSATKTFPNMNMENPWKVDPTIAADESFSQ 149
DB 81 LKFTVRDCSNIPNPGSKETFNLFYDESDDTSASNSPFWMENFYKVDTIAPDESFSK 140
QY 150 VDLGGRVKNINTEVRSGPVSRSFYLAFOQYGCMSLIAVRVRYKCPRIIQNGAIFQ 209
DB 141 LESG---RVNTKVRSFGPLSKNGFYLAFOQLGACMSLISVRAFYKCKSNTIAGFAIPE 196
QY 210 TLSGAESTSLVAARGSCIANAEEDVPTKLYCNGDGEWLVPIGRCMCKAGFEAVENGTV 269
DB 197 TLTGAETSLVIACTGCPINAVESVPLKLYCNGDGEWVPVGACTCAAGYEPAMKDTQC 256
QY 270 RGCPSGTFFKANQGDACHTCPIINSRTTSEGATNCVCRNGYYRADLDPLDMPTTIPSAQ 329
DB 257 QACGPGTFFKSKQGGPCSPCPNKRRTTAGAATVTCICRSGPFRADADPADSACTSVPSAPR 316
QY 330 AVISSVNETSLMLWTTPRDSGGREDLVYNIICKSCSGRGACTRCGDNVOYAPROL--- 386
DB 317 SVISNVNETSLVLEWSEFPQDAGGRDGLLYNVICKCKSVERRLCRCDNVEFVERQLGLT 376
QY 387 GLTEPRYISDLLAHTOYTFEIOAVNGVTDSPSPQFASVNTTNOAAPSAYSIMHOVS 446
DB 377 GLTERRYISKMAHPQTFEIOAVNGISSKSPPPHFPASVNTTNOAAPSVAFTMLHS 436
QY 447 RTVDSITLSWSQPPQNGVILDYELQYKE-LSEYNATAIKSPNTVTVOGLKAGAIYV 505
DB 437 STGNSMTLSWTPPRPNGLILDYBIKSEKQGGQDGIANTVTSQKNSVRLDGLKANARYM 496
QY 506 FOVPARTVAGRYSGRMVFTWTEAEVQTSIQEKLPLITGSSAAGVELIAVVVIAVC 565
DB 497 VQVPARTVAGRYSLPTFOTTAEDGSGTSTFOELPLIVGSATAGLLFVIVVIAVC 556
QY 566 NRRGF-----ERADSEYTDKLQHYTSGHMTGPMKIYIDPFTYDNEAVR 610
DB 557 FRKGMVTEQLSSPLGRKQRNSTDPEYTEKLQY---VTPGMKYIDPFTYDNEAVR 612
QY 611 EFAKEIDISCVKIEEYVIGAGEFGEVCRGLKLPGRREIFVAIKTLKSGYTEKQRDFLSE 670

; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatenIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645A-20

Query Match 70.6%; Score 3661.5; DB 2; Length 998;
Best Local Similarity 70.2%; Pred. No. 8.3e-264;
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

QY 10 LLLIPL-----AAVEETLMDSTTATAELGWMVHPSPGVEEYSGYDENMNTIRTVQCN 63
DB 23 LLLIPLLLPAGCRALLETMDTKWTSSELAWTSHPSGWEVSGYDEANPIRTYQCN 82
```



QY 601 TYEDPNEAVREFAKEIDISCVKIEOVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYT 660  
DB 613 TYEDPNEAVREFAKEIDVSCVKEEVIGAGEFGEVCRGLKQPGREEVVAIKTLKVGVT 672  
QY 661 EKQRDPLSEASIMGQFDHPNVIHLGVVTKSTPPWMIITEFMENGLSDFLRQNDQFTV 720  
DB 673 ERQRDPLSEASIMGQFDHPNVIHLGVVTKSTPPWMIITEFMENGLSDFLRQNDQFTV 732  
QY 721 IQLVGLRGTAAGKYLADNMYVHRDLAARNILVNSNLVKYSDFGLSRFLDSDPT 780  
DB 733 IQLVGLRGTAAGKYLSEWYVHRDLAARNILVNSNLVKYSDFGLSRFLDSDPT 792  
QY 781 TSALGGKIPIRWTAPEAIQYRKFTSADVMSYGIWVMEVMSYGERPYDMTQDVINAIE 840  
DB 793 TSSLGKIPIRWTAPEAIYRKFTSADVMSYGIWVMEVMSYGERPYDMTQDVINAIE 852  
QY 841 QYRLPPMDPCPSALHQLMDCWKORNRHPRKFGQIVNTLDMKIRNPNSLKAMAPLSSGI 900  
DB 853 QYRLPPMDPCPTALHQLMDCWVRDRNLPRKFSQIVNTLDMKIRNAASLKVIASQSGM 912  
QY 901 NLPLDRTIPDYSFNTVDWLEAIKMGQYKESFANAGFTSFVDSQMMEDILRLGVTL 960  
DB 913 SQPLDRTVPDYTFITVGDWLDKIMGRYKESFVSAGFASFDLVAQMTAEDILRLGVTL 972  
QY 961 AGHOKKILNSIQVMRAQMNQIOSVEV 986  
DB 973 AGHOKKILSSIQDMLRQMNQTLPVQV 998  
RESULT 14  
PCT-US95-04681-20  
; Sequence 20, Application PC/TUS9504681  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Amgen Patent Operations/RW  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04681  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 998 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-04681-20

Query Match 70.6%; Score 3661.5; DB 5; Length 998;  
Best Local Similarity 70.2%; Pred. No. 8.3e-264;  
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;  
QY 10 LALLPL-----AAVEETLMDSTTASLGMVWHPGWEVSGYDENMNTIRTYQVCN 63  
DB 23 LLLPLLLLPLAGRALEETLMDTKWTSELATWSHPESGWEEVSGYDEAMNPIRTYQVCN 82

QY 64 VPESQNNWLRTKFIERRGAHRHIVEMKFSVRDCSSIPSPVSGCKETFNLYYEADPDSA 123  
DB 83 VRESQNNWLRTGFIWRDDVQRVYVELKFTVRDCNSIPNIPGCKETFNLYYEADSDVA 142  
QY 124 TKTFNNMENPWKVDITIAADESFQVDLGRVNMKINTEVRSGPVSRSFYLAQDYGG 183  
DB 143 SASPFWMENPVYKVDITIADESPRLDAG---RVNTKVRSFQPLSKAGFYLAQDOGA 198  
QY 184 CMSLIAVRFVFKCPRIIONGAIQFQETLSGAESTSLVAARGSCIANAEEDVDVPIKLYCNG 243  
DB 199 CMSLISVRAFYKCASTTAGPALFPETLTGAETPSLVIAFGTCIPNAVESVPLKLYCNG 258  
QY 244 DGMVLPIGRCMCKAGFEAVENGTVCRGCPSGTFCANQDEACTHCPINRSTTSEGATNC 303  
DB 259 DGMWVPVGCATCATGHEPAKESQCRPCPPGSKAKQGEPCPLCPNPNRSTTSPAASIC 318  
QY 304 VCRNGYYPADLDLMPCTTIPSAPOAVISSVNETSLMELWTPPRDSGRDLVNNICK 363  
DB 319 TCHNPFYRADSADSACTTVPSPRGVISNWNSTSLLEWSEPRDLGVDRDLVNNICK 378  
QY 364 SC--GSGRGACTRCGDNVQYAPROLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFS 421  
DB 379 KCHGAGSASCRDDNVEFVPRQLGLSEPRVHTSHLLAHTRYTFEVQAVNGVSGKSLP 438  
QY 422 PQFASVNTTNOAPSIVSINHQVSRVTDSITLSWSQDQPNGVILDELOYKEKSEY 481  
DB 439 PRYAAVNTTNOAPSEVPTLRLHSSSGSLTSLWPPERPNGVILDEYKIFEK--SEG 496  
QY 482 NATAKSPNTVTVOGLKAGAIYVQVARTVAGYGRYGRMYFQMTME-AEYQTSIQEK 540  
DB 497 IASTVTSONSVQLDGLRDPDARYVQVARTVAGYGOYSRPAEFETTSESGAGQQLQEQ 556  
QY 541 LPLIIGSSAAGLVFLIAVAVIAVNCNRRGFERADSEYTDKLOHYTSGHMTQMKIYIDPF 600  
DB 557 LPLIVGSATAGLVFVAVVAVIAVCLRKORHSGSDSEYTEKLQY----IAPGMKYIIDPF 612  
QY 601 TYEDPNEAVREFAKEIDISCVKIEOVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYT 660  
DB 613 TYEDPNEAVREFAKEIDVSCVKEEVIGAGEFGEVCRGLKQPGREEVVAIKTLKVGVT 672  
QY 661 EKQRDPLSEASIMGQFDHPNVIHLGVVTKSTPPWMIITEFMENGLSDFLRQNDQFTV 720  
DB 673 ERQRDPLSEASIMGQFDHPNVIHLGVVTKSTPPWMIITEFMENGLSDFLRQNDQFTV 732  
QY 721 IQLVGLRGTAAGKYLADNMYVHRDLAARNILVNSNLVKYSDFGLSRFLDSDPT 780  
DB 733 IQLVGLRGTAAGKYLSEWYVHRDLAARNILVNSNLVKYSDFGLSRFLDSDPT 792  
QY 781 TSALGGKIPIRWTAPEAIQYRKFTSADVMSYGIWVMEVMSYGERPYDMTQDVINAIE 840  
DB 793 TSSLGKIPIRWTAPEAIYRKFTSADVMSYGIWVMEVMSYGERPYDMTQDVINAIE 852  
QY 841 QYRLPPMDPCPSALHQLMDCWKORNRHPRKFGQIVNTLDMKIRNPNSLKAMAPLSSGI 900  
DB 853 QYRLPPMDPCPTALHQLMDCWVRDRNLPRKFSQIVNTLDMKIRNAASLKVIASQSGM 912  
QY 901 NLPLDRTIPDYSFNTVDWLEAIKMGQYKESFANAGFTSFVDSQMMEDILRLGVTL 960  
DB 913 SQPLDRTVPDYTFITVGDWLDKIMGRYKESFVSAGFASFDLVAQMTAEDILRLGVTL 972  
QY 961 AGHOKKILNSIQVMRAQMNQIOSVEV 986  
DB 973 AGHOKKILSSIQDMLRQMNQTLPVQV 998

RESULT 15  
US-08-673-789-7  
; Sequence 7, Application US/08673789  
; Patent No. 5614479  
; GENERAL INFORMATION:  
; APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,  
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,  
; APPLICANT: GEORGE, F.

TITLE OF INVENTION: BSK RECEPTOR LIKE  
 TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR  
 TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC  
 TITLE OF INVENTION: METHODS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:

437	Db	NSMTLSWTPPERNGIIILDYEIKEYSEKOGODGIANTVTSQKNSVRDLDELKANARYMVQV	496
509	Qy	RARTVAGYGRYSKMYPQTTMEABYQTSIOEKLPLIICSSAAGLVFLIAVVVIAIVCNRR	568
497	Db	RARTVAGYGRYSLPTEFTQTTAEDGTSKTFQELPLIVGSATAGLLFVIVVVIIVCFCR	556
569	Qy	GFRADSEYTDKLQHYTSGHMTGPKYIIDPFTYEDDNEAVREFAKEIDISCVKIEQVIG	628
557	Db	QRNSTDPYETKLOQY----VTPGMKYIIDPFTYEDDNEAVREFAKEIDISCVKIEEVIG	612
629	Qy	AGSFEVCSGHKLPGKREIFVAIKTLKSGVTEKQRDFLSEASIMGQFDHPNVIHLEGV	688
613	Db	AGSFEVCRGRLLKUPGKREIFVAIKLUKVYTERQRDFLSEASIMGQFDHPNIIHLEGV	672
689	Qy	VTKSTPVMIIITFEMENGLSDSLFRQNDGQFTVIQLVGLMGRGIAAGMKYLADMYNVHRDLA	748
673	Db	VTKSRPVMIVTEEMENCALDSLFRLNDGQFTVIQLVGLMGRGIAAGMKYLSEMYNVHRDLA	732
749	Qy	ARNILVNSNLVCKVSDRGLSRPLEDDTSDPTYSALGGKPIRWTAPETAIQYRFTSASD	808
733	Db	ARNILVNSNLVCKVSDRGLSRPLEDDPADPTYSLSGGKPIRWTAPETAIYRFTSASD	792
809	Qy	VWSVGIIVMWEVMSYGERPYDMTNODVINAIEQDYRLPPPMDCPSALHQLMDCWKDRN	868
793	Db	VWSVGIIVMWEVMSYGERPYDMNSQDVINAVEQDYRLPPPMDCPTALHQLMDCWVRDRN	852
869	Qy	HRPKFGQIVNTLDKMIIRNPNSLKAAPLSSGINSPLPLDRITPYDTSFNTVDENLEAIKMG	928
853	Db	LRPKFAQIVNTLDKLIENAAASLKVIAVSQGVSPDLADRVDPYTTFTTGVGDWLDAIKMG	912
929	Qy	QYKESFANAQFTSPDVVSQMMEDIILRGVTLAGHQKILNSIOVMRAQNNQIOSVEV	986
913	Db	RYKENFVNHGAFSFDLVAQMTADLLRIGVTLAGHQKILSSIOQMLQNNQITLPVQV	970

```

; ; RNA ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY : UNKNOWN  
US-08-673-789-7
```

Query Match 69.6%; Score 3608.5; DB 2; Length 970;  
Best Local Similarity 70.1%; Pred. No. 7e+260;  
Matches 672; Conservative 116; Mismatches 161; Indels 9; Gaps 3;

QY		30 T A E L G W V H P S P G W E E Y S G D N E M N I T R T Y Q C V N F V S S Q N N U L K T F I R R R G A H R I H V E	89
		:   :	:
D b		21 T S E L A W T H E T G W E E Y S G Y D E A M Q P I R T Y Q C V R E A Q Q O W L R T F I N R Q D V Q R V Y V E	80
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
QY		90 M K F S V R D C S S I P S V P G S K E T F N I Y Y E A D P D S A T K T F P N M N M P W K V D T I A D E S F S Q	149
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
D b		81 L K F T V R D C K I P K I P G S K E T F N I F Y Y E S O T D S A S A N S P F M M N P Y I K V D T I A P D S F S K	140
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
QY		150 V D L G R V M K N T E V R S F G P V S R S G F Y L A F O D Y G C M S L I A V R V F R K C P R I I Q N G A L F O E	209
	:: ::  ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
D b		141 L E S G - - - - R V N T K V R S F G P L S K N G F Y L A F O D L G A C M S L I L V R A F Y K C S N T I A G F A I P P E	196
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
QY		210 T L S G A E S T S L V A A R G S C I A N A E E V D V P I K L Y C N G D G E W L V P I G R C M K A G P E A V E N G T V C	269
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
D b		197 T L T G A E P T S L V I A P G T C I P Q A V E S V P L K L Y C N G D G E W M V P V G A C T C A G Y E P A M K D T Q C	256
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
QY		270 R G C P S G T F K A N Q G D E A C H T C P I N S R T T S E G A T N C V C R N G Y Y R A D L D P L D M P C T T I P S A P Q	329
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
D b		257 Q A C P G T F K S Q G B G P C S P C P P N S R T T A G A A T V C I C R S G P P R A D A D P A D S A C T S V P S A P R	316
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
QY		330 A V T S S V N E T S I M L E W T P P R S G G R E D L V Y N I I C K S C S G R G A C T R C G N V O Y A P R Q I G L T	389
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
D b		317 S V I S N V N E T S F V L E W S P Q D A G G R D D L L Y N V I C K K S V E R L C S R C D D N V E F V P R Q I G L T	376
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
QY		390 E P R I Y S D L L A H T Q Y T F E I Q A V N G V T D Q S P F S P O F A S V N I T T N O A A P S A V S I M H Q V S R T V	449
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
D b		377 E R R I Y I S K W A H Q Y T F E I Q A V N G I S S K S P P P H F A S V N I T T N Q A V L S A V P T M L H S T G	436
		:   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~   :~	:
QY		450 D S I T L S W S Q D P N G V I L D Y E L Q Y Y E K E - L S E Y N N A T A I K S P T N T V T Q G L K A G A I Y V F Q V	508

Query Match	69.5%	Score	3603.5	DB 1	Length	993			
Best Local Similarity	68.5%	Fred. No.	1.7e-239						
Matches	680	Conservative	117	Mismatches	163	Indels	33	Gaps	6

  

QY	17	AAVEETLMDSTATTA-----ELGWMVHPGSGWEEVSGYDENNV	TIRTY	59
Db	11	AAAEFAAEATNSLILVRPTSEGRIDSEFVELAWTSHPSGWEVSA	YDEAMNPIRY	70
QY	60	QVCNVFSSQNNWLRTKFEIRRGARRHIVEMKFSVRDCSSIPSPGSK	ETFNLYYYEAD	119
Db	71	QVCNVRESSQNNWLRTGFIWRREVQVRVVELKFTVRDCNSIPNIPG	SKETFNLYFEAD	130
QY	120	FDSATKTFPNWENPWKVDVITAADESFQVDLGGRVNMIKINTVRS	FGPVSRSFYIAFQ	179

Db 131 SDVASASSPFWMENPYVVDIADESFSLDAG-----RVNKKVRSFGPLSKAGFYLAQ 186  
Qy 180 DYGGCMSLIAVRVYKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVVDVPIKL 239  
Db 187 DOGACMSLISVRAFYKCKASTAGFALFPETLTGAETSLVIAFGTCIANAVEVSVPLKL 246  
Qy 240 YCNGDGEWLVPICRCMKAGFEAVENGTVCRGCSGTFPKANQDEACTHCPINSRTTSEG 299  
Db 247 YCNGDGEWMVVGACTCATGHEPAKATQCRACPPGSKAKQEGCPCLPCPPNSRTTSPA 306  
Qy 300 ATNCVCRNGYVRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLVYN 359  
Db 307 ASICTCHNNFYRADSDTADSACTTVPSPPRGVSNVNETSLILEWSEPRDLGGDDLLYN 366  
Qy 360 IICKSCSGRGA-----CTRCGNVQYAPRQLGTEPRIYISDLLAHTQYTFEIQAVNGV 414  
Db 367 VICCKRSGSAGGAGPATCSRCDNVEPEPRQLGITERVHSHLLAHTRYTFEIQAVNGV 426  
Qy 415 TDQSPFPQFASVNITTNQAAPSIVSMHQVSRVDSITLSWSQDOPNGVILDYELQYY 474  
Db 427 SGKSPLPRVAANVITTNQAAPSEVPTLHSHSSGSSLTLSWAPPENGVILDYEMKYF 486  
Qy 475 EKELSEYNATAIKSPTTNTVVOGLKAGAIYVFOYRARTVAGYGRYSGWYFQMTWE-ABY 533  
Db 487 EK--SKGIASVTTSOKNSVQDGGQDPARYVYVQVARTVAGYGRYSPAEFTTSERGS 544  
Qy 534 QTSIQEKLPLIIGSSAGLVFLIAVWIAIVCNRRGFERADSEYTDKLQHYTSGHMTPGM 593  
Db 545 AQLQEQPLIVGSTVAGFVFMVVVIALVCLRKQRPDAEYTEKLOQY----VAPRM 600  
Qy 594 KIYIDPFTYEDPNBAVREFAKEIDISCVKIEQVITGAGEFGEVCSGHLKLPGRKIFVIAIK 653  
Db 601 KVIYIDPFTYEDPNBAVREFAKEIDVSCVKBIEVIGAGEFGEVCRGLKLPGRREVFVIAIK 660  
Qy 654 TLKSGYTEKORRDFLSEASINGQDHPNVHLEGVVTKSTPVMIIITFEMNGSLDSELRQ 713  
Db 661 TLKVGYTEKORRDFLSEASINGQDHPNIRLEGVVTKSRPVMIIITFEMNCALDSFLRL 720  
Qy 714 NDGQFTVQLVGLMGLGIAAGKYLADNMVYHRDLAARNILVNSLVCKVSDFGLSRFLD 773  
Db 721 NDGQFTVQLVGLMGLGIAAGKYLSEMMYVHRDLAARNILVNSLVCKVSDFGLSRFLD 780  
Qy 774 DTSOPTYTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIIVMEVMSYGERPVDWMTNQ 833  
Db 781 DPSDPTTSSLGKIPRTWTAPEAIDYRKFTSASDVMSYGIIVMEVMSYGERPVDWMTNQ 840  
Qy 834 DVINAIEQDYELPPMDCPSALHQLMDCQKDRNHPKFCQIVNTLDKMRNPNLSKAM 893  
Db 841 DVINAVEQDYELPPMDCPSALHQLMDCQKDRNHPKFCQIVNTLDKMRNPNLSKAM 900  
Qy 894 APLSSGINLPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVDVVSOMMEDI 953  
Db 901 ASAPSGMSQPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVDVVSOMMEDI 960  
Qy 954 LRLGVTLAGHOKTILNSIQVNRQMNQISVEV 986  
Db 961 LRLGVTLAGHOKTILNSIQVNRQMNQISVEV 993

## RESULT 18

US-09-192-435-1

; Sequence 1, Application US/09192435

; Patent No. 6303320

; GENERAL INFORMATION:

; APPLICANT: TAJIMA, HISAO

; APPLICANT: KITAGAWA, KOICHIRO

; APPLICANT: OHNO, HIROYUKI

; APPLICANT: UENO, TOSHIO

; TITLE OF INVENTION: A No. 6303320el Polypeptide of Protein p140

; TITLE OF INVENTION: and DNAs encoding it

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK &amp; SEAS

STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/09/192,435  
APPLICATION NUMBER: US/09/192,435  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/571,785  
FILING DATE: 13-DEC-1995  
APPLICATION NUMBER: 08/348,143  
FILING DATE: 23-NOV-1994  
APPLICATION NUMBER: JP 315806/1993  
FILING DATE: 24-NOV-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 993 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: rat  
TISSUE TYPE: skeletal muscle myoblast  
CELL LINE: L6  
US-09-192-435-1

Query Match 69.5%; Score 3603.5; DB 3; Length 993;

Best Local Similarity 68.5%; Pred. No. 1.7e-259;

Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;

Qy 17 AAVEETLMDSTTATA-----ELGMVHPSPGHEEVSVDENMTTIRTY 59  
Db 11 AAAAATAAATNSLSILVLRPTSEGRIDSEFVELAWTSHPESGHEEVSAYDEAMNPIRTY 70  
Qy 60 QVCNVPESSNNMLRTKFIERRGAHRITHVEMKFSVRDCSSIPSPVPGSKETENLYYYEAD 119  
Db 71 QVCNVRESSNNMLRTGFIWRREVQVRVVELKFTVRDCNSIPNIPGSKETFNLYFYEAD 130  
Qy 120 FDSATKTFPWNMPWVKVDITIAADESFQSDVLDGGRVYMKINTEVRSFSPVSRSGFYLAQ 179  
Db 131 SDVASASSPFWMENPYVVDIADESFSLDAG-----RVNKKVRSFGPLSKAGFYLAQ 186  
Qy 180 DYGGCMSLIAVRVYKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVVDVPIKL 239  
Db 187 DOGACMSLISVRAFYKCKASTAGFALFPETLTGAETSLVIAFGTCIANAVEVSVPLKL 246  
Qy 240 YCNGDGEWLVPICRCMKAGFEAVENGTVCRGCSGTFPKANQDEACTHCPINSRTTSEG 299  
Db 247 YCNGDGEWMVVGACTCATGHEPAKATQCRACPPGSKAKQEGCPCLPCPPNSRTTSPA 306  
Qy 300 ATNCVCRNGYVRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLVYN 359  
Db 307 ASICTCHNNFYRADSDTADSACTTVPSPPRGVSNVNETSLILEWSEPRDLGGDDLLYN 366  
Qy 360 IICKSCSGRGA-----CTRCGNVQYAPRQLGTEPRIYISDLLAHTQYTFEIQAVNGV 414  
Db 367 VICCKRSGSAGGAGPATCSRCDNVEPEPRQLGITERVHSHLLAHTRYTFEIQAVNGV 426  
Qy 415 TDQSPFPQFASVNITTNQAAPSIVSMHQVSRVDSITLSWSQDOPNGVILDYELQYY 474  
Db 427 SGKSPLPRVAANVITTNQAAPSEVPTLHSHSSGSSLTLSWAPPENGVILDYEMKYF 486





QY 774 DTSPTVTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWDMNQ 833  
DB 781 DPSPTVTSALGGKIPRTWTAPEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWDMNQ 840  
QY 834 DVINAISODYRLPPMDPCPSALHOLMLDCWQKORHHPKSGOIVNTLDMKIRNPNSLKAM 893  
DB 841 DVINAVSQDRLLPPMDPCPSALHOLMLDCWQKORHHPKSGOIVNTLDMKIRNPNSLKAM 900  
QY 894 APLSSGINLPLDRTIPDYTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSOMMEDI 953  
DB 901 ASAPSGMSQPLDRTIPDYTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSOMMEDI 960  
QY 954 LRIGVTLAGHOKKILNSIQVRAQMNQIQSV 986  
DB 961 LRIGVTLAGHOKKILNSIQVRAQMNQIQSV 993

RESULT 20  
US-08-162-809-8  
; Sequence 8, Application US/08162809  
; Patent No. 5457048  
; GENERAL INFORMATION:  
; APPLICANT: Pascuale, Elena B.  
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/162,809  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 9503  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 973 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-162-809-8

Query Match 64.4%; Score 3339.5; DB 1; Length 973;  
Best Local Similarity 63.1%; Pred. No. 7.5e-240;  
Matches 615; Conservative 150; Mismatches 197; Indels 13; Gaps 6;

QY 21 ETLMDSTATAELGCMVHPSPGMEVSGYDENMMNTIRYQVNCVFSSQNNWLRTKPIRR 80  
DB 3 ELLDTTGETSEIGTWSHPDGMEEVSRDDKERQIITFQVCNMDPEQNNWLRTKPIRR 62  
QY 81 RGAHRHVEKMFSPDCSSIPSPGSKCTFNLYYEADEFDSATKTPPNMNPWVKVD 140  
DB 63 RGAHRHVEKMFSPDCSSIPSPGSKCTFNLYYEADEFDSATKTPPNMNPWVKVD 122  
QY 141 IAADESESOVDLGRVNMKINTEVRSFGVSRSGFYLAFOYGGCMSLIAVRFVKCPRI 200  
DB 123 IAADESESOVDLGRVNMKINTEVRSFGVSRSGFYLAFOYGGCMSLIAVRFVKCPRI 162

QY 201 IQNGALFOETLSGAESTSLVAARGSCIANAEYDVP----IKLYCNGDGEWLVPIGRCMC 256  
DB 183 VKGFASFPETTFAGGERTSLVSLGTVCVANAEEASTTSSGSGVRLHNCGEWMTATGRSC 242  
QY 257 KAGFEAVENGTVCRCPSGTFKANOQDEACTHCPINSRT--TSEGATNCVCRNGYYRADL 314  
DB 243 KAGYQSDNENQAQACPIGSKASVGDGDCCLCPAHSHAPLPLFGTSEICQSCQSHYFAS 302  
QY 315 DPLDMPTCTTIPSAQAVISSVNETSLMLETTPRDSGGREDLVNIIKSCGS--GRGACT 373  
DB 303 DNSDAPCTGTPSPADLSYVIGSVNLLTWRLPKDLGGKDVFNVLCKPCPSRATCTV 362  
QY 374 RCGDNVOYAPRQLGLTEPRIYISDLLAHTOYTFEIQAVNGVTPQSPSPQFASVNIITNQ 433  
DB 363 RCGDNVOYAPRQLGLTEPRIYISDLLAHTOYTFEIQAVNGVTPQSPSPQFASVNIITNQ 422  
QY 434 AAPSAVSIHVSRTVDSITLSNSODPONGVILDYELQYKESLSYNATAKSPNTV 493  
DB 423 SVPSAIPMMHQSRTSSITLSWPQDPQNGVILDYELQYKESLSYNATAKSPNTV 482  
QY 494 TVOGLKAGAIYVQVARTVAGYGRYSGKMYFOTMTAEAYQTSIQEKLPLIISSAGLV 553  
DB 483 TIINLSPGKIYVQVARTVAGYGRYSGKMYFOTMTAEAYQTSIQEKLPLIISSAGLV 542  
QY 554 FLI--AVVIAIYCNRRGFERADSEYTDKLOHYTSGHMTGPKIYIDPFTYEDPNEAVRE 611  
DB 543 FLVIAAIALAIIFKSK--RRETPVTDRLQYISTRGL--GVKYIDPSTYEDPNEAVRE 598  
QY 612 FAKEDISCVKIEQVIGAGEFGEVCSGHLKPKGREIFVAKITLKSQYTKQRDFLSEA 671  
DB 599 FAKEDIVSFIKIEVIGAGEFGEVCSGHLKPKGREIFVAKITLKSQYTKQRDFLSEA 658  
QY 672 SIMQFDPHPNVIHLEGVWTKSTPMIITEPMENGLSDSFLRQNDQGTQVTLQVGLRGIA 731  
DB 659 SIMQFDPHPNVIHLEGVWTKSTPMIITEPMENGLSDSFLRQNDQGTQVTLQVGLRGIA 718  
QY 732 AGMKYLADMYVHRDLAARNILVNSNLVCKVSPDGLSRFLEDDTSDPTYSALGGKIPR 791  
DB 719 AGMKYLADMYVHRDLAARNILVNSNLVCKVSPDGLSRFLEDDTSDPTYSALGGKIPR 778  
QY 792 WTAPEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWDMNQVINAIDQYRLPPMD 851  
DB 779 WTAPEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWDMNQVINAIDQYRLPPMD 838  
QY 852 PSALHOLMLDCWQKORHHPKSGOIVNTLDMKIRNPNSLKAMAPLSSGINLPLDRTIPD 911  
DB 839 PTVLHLLMLDCWQKORHHPKSGOIVNTLDMKIRNPNSLKAMAPLSSGINLPLDRTIPD 898  
QY 912 YTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSOMMEDIILRLGVTLAGHOKKILNSI 971  
DB 899 FPSLSNAHEWLDKMGYKESFANAGFTSFVVSOMMEDIILRLGVTLAGHOKKILNSI 958  
QY 972 QVRAQMNQIQSV 986  
DB 959 QLMKVLHNLQLEPVEV 973

RESULT 21  
US-08-449-645A-13  
; Sequence 13, Application US/08449645A  
; Patent No. 5981245  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehaven Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA

QY 725 GMLRGIAGMKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRFLDSDTPTYSAL 784  
 DB 733 GMLRGIAGMKYLSDMGVYHRDLAARNILVNSLVCKVSDFGLSRFLDSDTPTYSAL 790  
 QY 785 GKKIPIRWTAPETATQYRKTFSASDVMSYGIWMEVMSYGERPYWDMTNQDVINAISQDIYR 844  
 DB 791 GKKIPIRWTAPETATQYRKTFSASDVMSYGIWMEVMSYGERPYWDMTNQDVINAISQDIYR 850  
 QY 845 LPPMDCPESALHQLMDCWQKDRNRHPRFGQIVNTLDMIRNPNLSLKAMAPLSSGINLPL 904  
 DB 851 LPPMDCPAALYQLMDCWQKDRNRHPRFGQIVNTLDMIRNPNLSLKAMAPLSSGINLPL 910  
 QY 905 LDRTPIDVTSTNTVDWLEAIKMQYKESFANAGFTSFVVSQMMEDILRLGVTLAQH 964  
 DB 911 AHSPLSGAYRSVGEWLEAIKMGRTYEIFWENGYSSMDAVAQVTLSDRLRLGVTLVGHQ 970  
 QY 965 KKLNSIQVMRAQM 978  
 DB 971 KKLNSIQVMRAQM 984

RESULT 22  
 US-08-702-367A-13  
 ; Sequence 13, Application US/08702367A  
 ; Patent No. 5981246  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fox, Gary M.  
 ; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
 ; TITLE OF INVENTION: Kinases  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 1840 Behavilland Drive  
 ; CITY: Thousand Oaks  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 91320  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/702,367A  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Winter, Robert B.  
 ; REFERENCE/DOCKET NUMBER: A-287  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 991 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-702-367A-13

Query Match 58.8%; Score 3053; DB 2; Length 991;  
 Best Local Similarity 58.8%; Pred. No. 1.6e-218; Indels 12; Gaps 9;  
 Matches 573; Conservative 165; Mismatches 224;  
 QY 6 LGALLLLPLLAAVEETLMDSTTATLGLMVMHPPSGWEVSGYDENMTIRTYQVCNVF 65  
 DB 22 LCAALRTLLASPSNEVLLDSRTVMGLGWIAFPKNGWEEIGVDENYAPIHTYQVCVM 81  
 QY 66 ESSQNNWLRTKPIRRGAHRIHVMKESVDCSSISVPSCSKETNLNLYYEAQFDSATK 125  
 DB 82 EQONQNNLLTSWISNEGASRIFELKFTLRDCNSLPGGLGTCKETFMWYFESDDQNGR- 140  
 QY 126 TFPNMENPWKVDITIAADESFQVLDLGRVMKINTEVRSFGVSRSGFYLAQDYGCCM 185  
 DB 141 ---NIKENQYIKIDITIAADESFTELDLGRVMKINTEVRSFGVSRSGFYLAQDVGACI 197

QY 725 GMLRGIAGMKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRFLDSDTPTYSAL 784  
 DB 733 GMLRGIAGMKYLSDMGVYHRDLAARNILVNSLVCKVSDFGLSRFLDSDTPTYSAL 790  
 QY 785 GKKIPIRWTAPETATQYRKTFSASDVMSYGIWMEVMSYGERPYWDMTNQDVINAISQDIYR 844  
 DB 791 GKKIPIRWTAPETATQYRKTFSASDVMSYGIWMEVMSYGERPYWDMTNQDVINAISQDIYR 850  
 QY 845 LPPMDCPESALHQLMDCWQKDRNRHPRFGQIVNTLDMIRNPNLSLKAMAPLSSGINLPL 904  
 DB 851 LPPMDCPAALYQLMDCWQKDRNRHPRFGQIVNTLDMIRNPNLSLKAMAPLSSGINLPL 910  
 QY 905 LDRTPIDVTSTNTVDWLEAIKMQYKESFANAGFTSFVVSQMMEDILRLGVTLAQH 964  
 DB 911 AHSPLSGAYRSVGEWLEAIKMGRTYEIFWENGYSSMDAVAQVTLSDRLRLGVTLVGHQ 970  
 QY 965 KKLNSIQVMRAQM 978  
 DB 971 KKLNSIQVMRAQM 984

Query Match 58.8%; Score 3053; DB 2; Length 991;  
 Best Local Similarity 58.8%; Pred. No. 1.6e-218; Indels 12; Gaps 9;  
 Matches 573; Conservative 165; Mismatches 224;  
 QY 6 LGALLLLPLLAAVEETLMDSTTATLGLMVMHPPSGWEVSGYDENMTIRTYQVCNVF 65  
 DB 22 LCAALRTLLASPSNEVLLDSRTVMGLGWIAFPKNGWEEIGVDENYAPIHTYQVCVM 81  
 QY 66 ESSQNNWLRTKPIRRGAHRIHVMKESVDCSSISVPSCSKETNLNLYYEAQFDSATK 125  
 DB 82 EQONQNNLLTSWISNEGASRIFELKFTLRDCNSLPGGLGTCKETFMWYFESDDQNGR- 140  
 QY 126 TFPNMENPWKVDITIAADESFQVLDLGRVMKINTEVRSFGVSRSGFYLAQDYGCCM 185  
 DB 141 ---NIKENQYIKIDITIAADESFTELDLGRVMKINTEVRSFGVSRSGFYLAQDVGACI 197  
 QY 186 SLIAVRFVRKPRIIQNGAFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDG 245  
 DB 198 ALVSRVYVYKCPVSRVLAHPDFTITGADSQLLEVSGCV-NHSVTDEPPKHCASRG 256  
 QY 246 EWLVPICGKCMKAGYEE-KNGI-CQVCRPGFFKASPHIQSCGKCPHYSYTHEEASTSCVC 314  
 DB 257 EWLVPICGKCMKAGYEE-KNGI-CQVCRPGFFKASPHIQSCGKCPHYSYTHEEASTSCVC 314  
 QY 306 RNYGYPADLDPLDMPCTTIPSPAPQAVISVNETSLMLEWTPRDSGGREDLVNLIKSC 365  
 DB 315 EKDYFRRESDPPTMACTRPSPAPRAISVNETSVFLEWIPPADTGGKRDVSYIACKKC 374  
 QY 366 GSGRGACTCGDNVOVAPRLGLTEPRIYISDLAHTQVTEIQAQVNGVTQSPSPQFA 425  
 DB 375 NSHAGVCECGHVRVLPQSGLKNTSVNMDLLAHTNFTFEIAGVNGVSDLSGPARQYV 434  
 QY 426 SVNITTQAAPSASVIMHVSRTVDSITLSWSQOPQNGVILDYELQYKELSEYNATA 485  
 DB 435 SVNITTQAAPSPTNVKGIKAKNGISLSWQEPDRPNNGIILEYIKHFKED-QETSITI 493  
 QY 486 IKSPNTVTVQGLKAGAIYVQVARTVAGYSGKMYFOTWTAETYSIQEKLPLII 545  
 DB 494 IKSKETTITAEGLKPAVYVQIRATAGYVFSRFEFET-TPVFAASSQSQIPVIA 552  
 QY 546 GSSAAGLVFLIAVVAIVCNRRGFRADSEYTDKLQHYTSGHM-TPGMKIIYIDPFTYED 604  
 DB 553 VSVTVGVILLAVIGVLLSGRRGYSKAKQDPEEKMHFNHGHILKPGVTVTIDPFTYED 612  
 QY 605 PNEAVREFAKEIDISCVKIQQVIGAGEFVCSGHLKLPCKREIFVAIKTLKSGYTEKOR 664  
 DB 613 PNOAVHEFAKEIEASCTIERVIGAGEFVCSGRLKLPCKRELPAIKTLKSGYTEKOR 672  
 QY 665 RDLSEASIMQDFPHNVHLEGVVTKSTPMVITIFEMENGSLDSFLRQNDQFTVIQLV 724  
 DB 673 RDLSEASIMQDFPHNIHLEGVVTKSTPMVITIFEMENGSLDSFLRQNDQFTVIQLV 732



Db 733 GMLRGISAGMKYLDGMYVHRDLAARNILNSLVCKVSDFGLSRVLEDD-PEAAVYTR- 790  
Qy 785 GGIPIRTAPEALQVRKFTSASDVMSYGVIMVMSYGERPYWDMTNDQVINAIBQDYR 844  
Db 791 GGIPIRTAPEALQVRKFTSASDVMSYGVIMVMSYGERPYWDMTNDQVINAIBQDYR 850  
Qy 845 LPPMDCPALHQLMDCWQKRNHRPKFQIIVNTLDKMRNPSNLKAMAPLSSGINLPL 904  
Db 851 LPPMDCPALHQLMDCWQKRNHRPKFQIIVNTLDKMRNPSNLKAMAPLSSGINLPL 910  
Qy 905 LDRTPYTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSOMMEDILRLGVTLGHQ 964  
Db 911 AHSPLGSGAYRSVGEWLEAKMGQYKESFANAGFTSFVVSOMMEDILRLGVTLGHQ 970  
Qy 965 KKLNSIQVMRAQM 978  
Db 971 KKLNSIQVMRAQM 984

RESULT 24  
US-08-449-645A-30  
; Sequence 30, Application US/08449645A  
; Patent No. 5981245  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,645A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 967 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-449-645A-30

Query Match 58.8%; Score 3049; DB 2; Length 967;  
Best Local Similarity 59.0%; Pred. No. 3.1e-218;  
Matches 572; Conservative 165; Mismatches 219; Indels 14; Gaps 10;

Qy 12 LPLLAALV--EETLMDSTATAELGMMVHPSPGMEVSGYDENMNTIRTYQVNVFSSQ 69  
Db 2 LPLLAALV--EETLMDSTATAELGMMVHPSPGMEVSGYDENMNTIRTYQVNVFSSQ 61  
Qy 70 NNLWRTKTRRRGAHRIHVMKFSVDCSSIPSVGSKETFNLYVEADPDSATKTPN 129  
Db 62 NNLWRTKTRRRGAHRIHVMKFSVDCSSIPSVGSKETFNLYVEADPDSATKTPN 117  
Qy 130 WNNPWWYDTTAADESFSQVLDGGRVKNINTEVASFVSRSGFYLAQDYGGMSLIA 189  
Db 118 IKENQVKKIDTAADESFTLDDGGRVKNINTEVASFVSRSGFYLAQDYGGMSLIA 177  
Qy 190 VRFVYKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWL 249

Db 178 VVVYKCPRIITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWL 236  
Qy 250 FIGRCMKAGFEAVNGVTCVCGSPGTGKAGQDEACHTCPINRTTSEGATNCVCRNGY 309  
Db 237 FIGRCMKAGFEAVNGVTCVCGSPGTGKAGQDEACHTCPINRTTSEGATNCVCRNGY 294  
Qy 310 YRADIPLDMCTTTPSAPOAVISSVNETSLMELWTPRDSGGREDLVYNIICKSCSGSR 369  
Db 295 FRRESDPPTMACTRPSPAPRNAISNVNETSVLEWIPADTGGKDVYIYACKCNSHA 354  
Qy 370 GACTRCGDNVQYAPQLGTEPRIYISDLAHTQVTFEIQAVNGVTDSPSPQASVNI 429  
Db 355 GVCESCGHVRVLPQSGKNTSVMMVLLAHTNYTFEIEAVNGVSDLSPGARQVSVNV 414  
Qy 430 TTNQAAPSAVSMHVOVSRVDSITLSWQDPDNGVILDYLOVYVEKELSEYNATAIKSP 489  
Db 415 TTNQAAPSAVSMHVOVSRVDSITLSWQDPDNGVILDYLOVYVEKELSEYNATAIKSP 473  
Qy 490 TTNVTVQGLKAGAIYVFOVARTVAGYGRYSGKMYFOTWTEAEYQTSIQEKLPLIGSSA 549  
Db 474 ETITTAAGLKPASVIVFQIRARTAGYGVFSRPFET-TPVFAASSDQSQIPVIAVST 532  
Qy 550 AGLVFLIAVVIIVCNRRGFERADSEYTDKLQHTSGHM-TPGMKIYIDPETYEDPNEA 608  
Db 533 VGVILLAVVIGVLLSGRCYSGAKQDPEEKXMHFNHGHILPGVRTYIDPHTYEDPNEA 592  
Qy 609 VREFAKEIDISCVKLEQVIGAGEFGEVCSGHLKPKREIFVAIKTLKSGYTEKQRRDPL 668  
Db 593 VHEFAKEIEASCITIERVIGAGEFGEVCSGHLKPKREIFVAIKTLKSGYTEKQRRDPL 652  
Qy 669 SEASIMQGFDPHNPVHLEGVVTSTPMIITBFMENGSLDSFLRQNDGQFTVQLVGMRL 728  
Db 653 GEASIMQGFDPHNPVHLEGVVTSTPMIITBFMENGSLDSFLRQNDGQFTVQLVGMRL 712  
Qy 729 GIAAGKYLADMYVHRDLAARNILNSLVCKVSDFGLSRVLEDD-PEAAVYTR-GGKI 788  
Db 713 GISAGMKYLDGMYVHRDLAARNILNSLVCKVSDFGLSRVLEDD-PEAAVYTR-GGKI 770  
Qy 789 PIRWTAPEALQVRKFTSASDVMSYGVIMVMSYGERPYWDMTNDQVINAIBQDYR 848  
Db 771 PIRWTAPEALQVRKFTSASDVMSYGVIMVMSYGERPYWDMTNDQVINAIBQDYR 830  
Qy 849 MDCPSALHQLMDCWQKRNHRPKFQIIVNTLDKMRNPSNLKAMAPLSSGINLPLDRT 908  
Db 831 MDCPSALHQLMDCWQKRNHRPKFQIIVNTLDKMRNPSNLKAMAPLSSGINLPLDRT 890  
Qy 909 IPDYTSFNTVDEWLEAKMGQYKESFANAGFTSFVVSOMMEDILRLGVTLGHQKIL 968  
Db 891 PLGSGAYRSVGEWLEAKMGQYKESFANAGFTSFVVSOMMEDILRLGVTLGHQKIL 950  
Qy 969 NSIQVMRAQM 978  
Db 951 NSIQVMRAQM 960

RESULT 25  
US-08-702-367A-30  
; Sequence 30, Application US/08702367A  
; Patent No. 5981246  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,367A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 967 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-702-367A-30

Query Match 58.8%; Score 3049; DB 2; Length 967;  
Best Local Similarity 59.0%; Pred. No. 3.1e-218;  
Matches 572; Conservative 165; Mismatches 219; Indels 14; Gaps 10;  
  
Qy 12 LLPLLAIV--EETLMDSTTAAELGWMVHPPSGWEEVSGYDENNTTIRTYQVCNVFESSQ 69  
Db 2 LRTLLASPSNEVLLDSRTVMGDLGWIATFAPKNGWEEIGEVNDENYAPHTTYQVCKVMEQNG 61  
  
Qy 70 NNWLRTFIERRGAHRHIVEMKFSVRDSSIPSPVSGCKETFNLYYEADPDSATKTFPN 129  
Db 62 NNWLLTSWISNEGASRIFELKFTLRDCNSLPGGLGCTKFTNNYFESDDQNGR----N 117  
  
Qy 130 WMENPVKVDITIAAESFSDVLGGVYKINTEVRSFGPVSRSGFYLAFOYDGCMSLIA 189  
Db 118 IKENQYIKIDTIADESFTLDELGDRVMKINTEVDRVGLSKGKGYLAFOYDVGACIALVS 177  
  
Qy 190 VRVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPILKLYCNGDGEMLV 249  
Db 178 VRVYKCKPSVVRHLAVFPDITITGADSSQLLEVSQV-NHSTVDDEPPKMHCSAEGEWLV 236  
  
Qy 250 PIGRCMKAGFEAVENGTVRCGCPSTGTFKANQGDCACTHCPINSTRTSSEGAATNCVNGY 309  
Db 237 PIGRCMKAGYEE-KNGT-CQVCRPGFKASPHIQSCGKCPHSHYTHEEASTSCVCEKDY 294  
  
Qy 310 YRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSSGGREDLVNIIKSCGSGR 369  
Db 295 FRRESDPPTWACTRPPSAPRNAINSVNETSVFLEWIPADTGGKDVSYIACKKCNSHA 354  
  
Qy 370 GACTRCGDNVQYAPROLGLTEPRYIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 429  
Db 355 GVCBECGHRVYLPQSGLKNTSMVMVDLLAHTNYTTFEIEAVNGVSDLSFGARQYVSVNV 414  
  
Qy 430 TTNOAAPSANVIMHOVSRTVDSITLSQSDQPNQNGVILDYELQYKELSEYNATAIKSP 489  
Db 415 TTNOAAPSPTNVKKGKIANKSISLSQEPDRPNGIILEYIKHFEXD-QETSYTIKSK 473  
  
Qy 490 TINTVVOGLKAGALYVFOVQARTVAGYGRYSGKMYFOTMTEAEYQTSIQEKLPLIGSSA 549  
Db 474 ETTITAGLKPASVYVQIARTAAAGYGVSRREFET-TPVFASSDQSQIPIVAVSVT 532  
  
Qy 550 AGLVFLIAVVIAVCNRRGFERADSEYTKLQHYTSGHM-TPGMKIYIDPFTYEDPNEA 608  
Db 533 VGVILLAVIGVLLSGRRGYSKAKQDPEEKMHFNHGIKLPGRVYIDPHTYEDPNQA 592  
  
Qy 609 VREPAKIDISCVKIEQVIGAGEGECVSHGLKLPGRKEIFVAIKTKSGYTEKQRDPL 668  
Db 593 VHEPAKIEASCITIERVIGAGEGECVSGRLKLPGRKRELVAIKTKLVGYTEKQRDPL 652  
  
Qy 669 SEASIMGOFDHPNVIHLEGVVTKTTPVMIITERMENGLSDSFLRNDQGFVILQVGLMR 728  
Db 653 GEASIMGOFDHPNIIHLEGVVTKSPVMIITERMENGLSDTFLKNDQGFVILQVGLMR 712  
  
Qy 729 GIAAGMKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRFLBDDTSDPTTYSALGGKI 788

Db 713 GISAGMKYLSDMGYVHRDLAARNILVNSLVCKVSDFGLSRVLEDD-PEAAVTTT-GGKI 770  
Qy 789 PIERTAPEALQYKFTSASDVMSYGVIMVMSYGERPYWDMTNQDVINAIEQDYRLPPP 848  
Db 771 PIERTAPEALAFKFTSASDVMSYGVIMVMSYGERPYWDMTNQDVIKAVEGYRUPSP 830  
Qy 849 MDCPSALHQLMLDCWQKDRNHRPKFQIVNTLDMIRNPNLSLKAMAPLSSGILPLLDRT 908  
Db 831 MDCPAALYQLMLDCWQKERNRPFDEIVNMLDKLIRNPSSLKTLVNASCRVSNLLAHS 890  
Qy 909 IPDYSFNTVDEWLEAIKMGQYKESFANAGFTSFVVVSQMMEDILRLGVTLAGHQKIL 968  
Db 891 PLGSGAYRSVGEWLEAIKMGRYTEIFPMENGYSMDAVAQVTLDELRLRLGLVTLGHQKKIM 950  
Qy 969 NSIQVMRAQM 978  
Db 951 NSLQEMKVL 960  
  
RESULT 26  
US-09-751-389-7  
; Sequence 7, Application US/09751389  
; Patent No. 6630334  
; GENERAL INFORMATION:  
; APPLICANT: GUEGLER, Karl et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: C001067  
; CURRENT APPLICATION NUMBER: US/09/751,389  
; CURRENT FILING DATE: 2001-01-02  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 953  
; TYPE: PRT  
; ORGANISM: Human  
US-09-751-389-7  
  
Query Match 58.8%; Score 3048; DB 4; Length 953;  
Best Local Similarity 59.2%; Pred. No. 3.6e-218;  
Matches 568; Conservative 164; Mismatches 216; Indels 12; Gaps 9;  
  
Qy 20 EETLMDSTTAAELGWMVHPPSGWEEVSGYDENNTTIRTYQVCNVFESSQNNWLRKFI 79  
Db 3 EVNLLDSRTVMGDLGWIATFAPKNGWEEIGEVNDENYAPHTTYQVCKVMEQNNWLLTSWIS 62  
  
Qy 80 RRGARHIVEMKFSVRDSSIPSPVSGCKETFNLYYEADPDSATKTFPNNMENPVKVD 139  
Db 63 NEGASRIFELKFTLRDCNSLPGGLGCTKFTNNYFESDDQNGR----NIKENQYIKID 118  
  
Qy 140 TIAADESFSDVLGGVYKINTEVRSFGPVSRSGFYLAFOYDGCMSLIAVRVYRKCP 199  
Db 119 TIAADESFTELDELGDRVMKINTEVDRVGLSKGKGYLAFOYDVGACIALVSVRVYRKCP 178  
  
Qy 200 IIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPILKLYCNGDGEMLVPIGRCKMCKAG 259  
Db 179 VVRHLAVFPDITITGADSSQLLEVSQV-NHSTVDDEPPKMHCSAEGEWLVPIGRCKMCKAG 237  
  
Qy 260 FEAVENGTVRCGCPSTGTFKANQGDCACTHCPINSTRTSSEGAATNCVNGYRADLDPLDM 319  
Db 238 YEE-KNGT-CQVCRPGFKASPHIQSCGKCPHSHYTHEEASTSCVCEKDYFRRESDDPTM 295  
  
Qy 320 PCTTISAPQAVISSVNETSLMLEWTPPRDSSGGREDLVNIIKSCSGSGACTRCGDV 379  
Db 296 ACTRPPSAPRNAINSVNETSVFLEWIPADTGGKDVSYIACKKCNHAGVCEECGGHV 355  
  
Qy 380 QYAPROLGLTEPRYIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNTTNOAAPS 439  
Db 356 RYLPGRGLKNTSMVMVDLLAHTNYTTFEIEAVNGVSDLSFGARQYVSVNTTNOAAPS 415  
  
Qy 440 SIMHOVSRTVDSITLSQSDQPNQNGVILDYELQYKELSEYNATAIKSPNTTNTVVOGLK 499





		NAME: Winter, Robert B.	
		REFERENCE/DOCKET NUMBER: A-287	
		INFORMATION FOR SEQ ID NO: 15:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 986 amino acids	
		TYPE: amino acid	
		TOPOLOGY: linear	
		MOLECULE TYPE: protein	
		US-08-702-367A-15	
		Query Match	58.7%; Score 3045; DB 2; Length 986;
		Best Local Similarity	59.3%; Pred. No. 6.4e-218;
		Matches	580; Conservative 146; Mismatches 212; Indels 40; Gaps 12;
Qy	18	AVEETLMDSTTATAELGWMVHP-PSGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTK	76
Db	28	ANEVTLLDSRSVQGLGWIASPLEGGWEVSIIMDEKNTPIRTYQVCNVFESSQNNWLRTD	87
Qy	77	FIRRGARHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFDSDATKTFPNWMPV	136
Db	88	WITREGARVIEIKTLRDCNSLPGVMGCKETFNLYYESDNDKERFI-----RENQFV	143
Qy	137	KVDITAADESFOVDLGRVNMKINTEVRSPGSKETFNLYYEADFDSDATKTFPNWMPV	196
Db	144	KIDITAADESFTQVDIGDRIMKLNTEIRDVGPLSKGFLAFQDVGACIALVSRVFYK	203
Qy	197	CPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPICRCMC	256
Db	204	CPLTVRLNAQPPDITIGADTSSLVVRGSCVNNSEKDV-PMYCGADGEWLVPICNCLC	262
Qy	257	KAGFEAVENGIVCGSGTPEKANKQDEACTHCPIINSRTTSEGATNCVCRNGYYRADLDP	316
Db	263	NAGHE--ERSGEQACKIGYKALSTDTATCAKCPHYSVWEGATSCDGRGFRADNDA	320
Qy	317	LDMPCTTIPSAQAVISSVNETSIMLEWTPPRDSGGREDLVNIIKSCSG-RCGATRC	375
Db	321	ASMPCTPPSAPLNLISNVNETSVNLEWSSPQNTGGRQDISYNVVKCKGAGDPKCRPC	400
Qy	376	GNVOYAPROGLTEPRIYISDLAHTQYTEIOAVNGVTDOSPFPQFASVNTNQAA	435
Db	381	GSQVHTPQNGLTKTKVTSITDLAHTNYTEIWAIVNGSVKYNPNPQSVSVTTNQAA	440
Qy	436	PSAVSIHQVSRVDSITLSQSDOPNGVILDYELQYKELSEYNATAIKSPNTVTV	495
Db	441	PSIALVQAEKTRYSVALAWLEDPDRPNGVILEVYKEDQNSRVIRVTAARNDI	500
Qy	496	QCLKAGAIYFQVARTVAGYGRYGRMYQTMTEAEYQTSIQEKL-PIIGS-----	547
Db	501	KGLNELTSYVHVHARTAAAGYDFSEPLEVTNT-----VPSRIIGDGANSTVL	549
Qy	548	--SAGLVFLTAVVIAVCHRR--GPERADSEYTDKLOHTSGHMTPGMKIYIDPPTYE	603
Db	550	LVSVSGSVVLVILLAAVFISSRSKYSKAKQEADEE-----KHLNGQVTVDPPTYE	603
Qy	604	DNEAVREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRRI FVAIKTLKSGYTEKQ	663
Db	604	DNQAVREFAKEIDASCIEKIVGFEVGEVCSGRLKVPKREICVAIKTLKAGYTDKQ	663
Qy	664	RDFLTSEASIMQFDPNVIHLEGVVTKSTPMTIPEWNGSLDSFLRNDGSOFTVIOL	723
Db	664	RDFLTSEASIMQFDPNIIHLEGVVTKSTPMTIPEWNGSLDFAFLRKNDGFTVIOL	723
Qy	724	VGMLRGIAGMKYLDAMNVHRDLAARNILVNSNLVCKVSPFGLSRFLEDDTSDPTTSA	783
Db	724	VGMLRGIAGMKYLDMSVHRDLAARNILVNSNLVCKVSDFGMSRVLEDD-PEAAVYTR	782
Qy	784	LGKIPIRWTAPEAIQYRKFTSASDVWSYGIWVWVMSYGERPYWDMNQDVINAIEDQY	843
Db	783	-GKIPIRWTAPEAIYRKFTSASDVWSYGIWVWVMSYGERPYWDMNQDVKAIEBEGY	841
Qy	844	RLPPMDCFSALHOLMDCQWRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLP	903
Db	842	RLPPMDCFIALHQLMDCQWERSDRPKFGQIVNMLDKLIRNPNLSKRTGTSSRPNTA	901





**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 16:32:55 ; Search time 210 Seconds  
(without alignments)  
2701.521 Million cell updates/sec

Title: US-09-914-883-2  
Perfect score: 5188  
Sequence: 1 MALRRIGALLLLPLLAIVE.....ILNSIQVMRAQMNQIOSVEV 986

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5184	99.9	1055	1	EPB2_HUMAN
2	5168	99.6	1021	2	Q6GTQ7
3	5157.5	99.4	1029	2	Q6P5F1
4	5157.5	99.4	1029	2	AAH62924
5	5130	98.9	994	1	EPB2_MOUSE
6	4975.5	95.9	1004	1	EPB2_CHICK
7	4945	95.3	987	1	EPB2_COTUJA
8	3934.5	75.8	984	1	EPB1_RAT
9	3930.5	75.8	984	2	Q8CBF3
10	3924	75.6	984	1	EPB1_HUMAN
11	3916.5	75.5	984	2	Q6PG23
12	3916.5	75.5	984	2	AAH57301
13	3767	72.6	985	1	EPBA_XENLA
14	3753.5	72.3	815	2	O57458
15	3721	71.7	984	1	EPB1_CHICK
16	3705	71.4	943	2	Q8CB22
17	3670.5	70.7	998	2	Q7Z740
18	3662.5	70.6	998	1	EPB3_CHICK
19	3661.5	70.6	998	1	EPB3_HUMAN
20	3657.5	70.5	993	2	Q91Y59
21	3630.5	70.0	993	1	EPB3_MOUSE
22	3612.5	69.6	902	1	EPBB_XENLA
23	3489	67.3	974	2	Q6NR59
24	3489	67.3	974	2	AAH70804
25	3485	67.2	974	1	EPB3_XENLA
26	3480	67.1	974	2	Q6DGF4
27	3441	66.3	938	2	Q60669
28	3354.5	64.7	1002	1	EPB5_CHICK
29	3235	62.4	923	2	Q90ZN8
30	3085	59.5	986	1	EP4A_XENLA
31	3080	59.4	986	2	Q7ZYM7

32	3075.5	59.3	985	1	EP4B_XENLA
33	3065.5	59.1	986	1	EP4A_CHICK
34	3045	58.7	986	1	EP4A_HUMAN
35	3043	58.7	986	2	Q8OVZ2
36	3040	58.6	986	1	EP4A_MOUSE
37	3038.5	58.6	993	1	EP4A_CHICK
38	3036	58.5	1037	1	EP4A_HUMAN
39	3028	58.4	998	1	EP4A_HUMAN
40	3017	58.2	998	2	Q8BSU8
41	3013	58.1	998	1	EP4A_MOUSE
42	3013	58.1	998	1	EP4A_RAT
43	3010.5	58.0	969	2	Q7Z3F2
44	3009	58.0	1013	1	EP4A_CHICK
45	3006	57.9	994	2	Q8R381
46	2969	57.2	976	2	Q90ZN9
47	2959.5	57.0	927	2	Q99KA8
48	2931	56.5	983	1	EP4A_CHICK
49	2930.5	56.5	983	1	EP4A_HUMAN
50	2928	56.4	984	2	Q8BRE1
51	2928	56.4	984	2	Q8C3U1
52	2925.5	56.4	983	2	Q6PAR6
53	2925.5	56.4	983	2	AAH63282
54	2923	56.3	1005	1	EP4A_RAT
55	2914	56.2	984	1	EP4A_MOUSE
56	2887.5	55.7	983	1	EP4A_MOUSE
57	2863.5	55.2	987	2	Q99MR2
58	2860.5	55.1	987	2	Q8C7S3
59	2860	55.1	981	1	EP4A_BRARE
60	2856.5	55.1	987	2	Q91YM0
61	2854.5	55.0	987	1	EP4A_MOUSE
62	2854	55.0	996	2	Q8C8K1
63	2844	54.8	987	1	EPB4_HUMAN
64	2844	54.8	987	2	AAH14194
65	2843.5	54.8	552	2	Q9H4H4
66	2843	54.8	987	2	Q7Z635
67	2839.5	54.7	621	2	Q9H4H3
68	2809.5	54.2	1035	1	EP4A_MOUSE
69	2743.5	52.9	987	2	Q73875
70	2712.5	52.3	1005	1	EP4A_HUMAN
71	2696.5	52.0	880	2	Q73879
72	2681	51.7	976	2	Q73878
73	2674	51.5	1004	1	EP4A_MOUSE
74	2654	51.2	935	2	Q96L35
75	2599.5	50.1	948	1	EP4A_RAT
76	2545	49.1	482	2	Q6NVM1
77	2545	49.1	482	2	AAH67861
78	2485.5	47.9	864	2	Q6K580
79	2467	47.6	1014	2	Q8K0A9
80	2465	47.5	1014	2	Q8BN76
81	2464	47.5	877	1	EP4A_MOUSE
82	2463	47.5	1014	1	EPB6_MOUSE
83	2461	47.4	1006	1	EPB6_HUMAN
84	2461	47.4	1006	1	AAH20939
85	2391	46.1	819	2	Q6PFV6
86	2391	46.1	819	2	AAH57401
87	2389.5	46.1	818	2	Q6KF79
88	2370.5	45.7	976	2	Q8N3Z2
89	2357	45.4	977	1	EP4A_MOUSE
90	2356.5	45.4	976	1	EP4A_HUMAN
91	2343.5	45.2	974	2	Q6DI14
92	2318.5	44.7	976	2	Q6NTV5
93	2318.5	44.7	976	2	AAH68849
94	2313.5	44.6	977	2	Q9PWR5
95	2272.5	43.8	1011	2	Q6VU50
96	2272.5	43.8	1011	2	AAQ87231
97	2236	43.1	984	2	Q6NZS1
98	2236	43.1	984	2	AAH65990
99	2069	39.9	1003	2	Q95YL0
100	2051.5	39.5	969	2	Q98TD0

ALIGNMENTS

RESULT 1  
EPB2\_HUMAN  
ID EPB2\_HUMAN STANDARD; PRT; 1055 AA.  
AC P29323; O43477;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein  
DE kinase receptor EPH-3) (DRT) (Receptor protein-tyrosine kinase HEK5  
DE (ERK).  
GN Name=EPHB2; Synonyms=EPTB3, ERK, DRT, HEK5;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RC TISSUE=Fetal brain;  
RX MEDLINE=96154673; PubMed=8589679;  
RA Ikegaki N., Tang X.X., Liu X.-G., Biegel J.A., Allen C., Yoshioka A.,  
RA Sulman E.P., Brodeur G.M., Pleasure D.E.;  
RT "Molecular characterization and chromosomal localization of DRT  
RT (EPH3): a developmentally regulated human protein-tyrosine kinase  
RT gene of the EPH family.";  
RL Hum. Mol. Genet. 4:2033-2045(1995).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RC TISSUE=Gastric carcinoma;  
RX MEDLINE=93343925; PubMed=7688222;  
RA Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.;  
RA "Identification of protein-tyrosine kinase genes preferentially  
RA expressed in embryo stomach and gastric cancer.";  
RL Biochem. Biophys. Res. Commun. 194:698-705(1993).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM LONG).  
RC TISSUE=Fetal brain;  
RX MEDLINE=98359217; PubMed=9696046;  
RA Tang X.X., Pleasure D.E., Brodeur G.M., Ikegaki N.;  
RA "A variant transcript encoding an isoform of the human protein  
RA tyrosine kinase EPHB2 is generated by alternative splicing and  
RA alternative use of polyadenylation signals.";  
RL Oncogene 17:521-526(1998).  
RN [4]  
RP SEQUENCE OF 15-986 FROM N.A. (ISOFORM SHORT).  
RC TISSUE=Brain;  
RX MEDLINE=95206782; PubMed=7898931;  
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,  
RA Basu R., Welcher A.A.;  
RT "cDNA cloning and tissue distribution of five human EPH-like receptor  
RT protein-tyrosine kinases.";  
RL Oncogene 10:897-905(1995).  
RN [5]  
RP SEQUENCE OF 509-986 FROM N.A. (ISOFORM SHORT).  
RC TISSUE=Fetal brain;  
RX PubMed=7601466;  
RA Saito T., Seki N., Mateuda Y., Kitahara M., Murata M., Kanda N.,  
RA "Identification of the human ERK gene as a putative receptor tyrosine  
RA kinase and its chromosomal localization to lp36.1: a comparative  
RA mapping of human, mouse, and rat chromosomes.";  
RL Genomics 26:382-384(1995).  
RN [6]  
RP SEQUENCE OF 652-712 FROM N.A.  
RX MEDLINE=91296384; PubMed=1648701;  
RA Chan J., Watt V.M.;  
RT "eek and erk, new members of the eph subclass of receptor protein-  
RT tyrosine kinases.";  
RL Oncogene 6:1057-1061(1991).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-986 (ISOFORM SHORT).  
RX MEDLINE=99132419; PubMed=9933164;  
RA Thanos C.D., Goodwill K.E., Bowie J.U.;

"Oligomeric structure of the human EphB2 receptor SAM domain.";  
Science 283:833-836(1999).  
CC -1- FUNCTION: Receptor for members of the ephrin-B family.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBUNIT: The ligand-activated form interacts with multiple  
CC proteins, including GTPase-activating protein (RASGAP) through its  
CC SH2 domain. Binds RASGAP through the juxtamembrane tyrosines  
CC residues. Interacts with PRKCBP and GRIP1 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Name=Long; Synonyms=EPHB2V;  
CC IsoId=P29323-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=P29323-2; Sequence=VSP\_003016, VSP\_003017;  
CC -1- TISSUE SPECIFICITY: Brain, heart, lung, kidney, placenta,  
CC pancreas, liver and skeletal muscle. Preferentially expressed in  
CC fetal brain.  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
CC receptor subfamily.  
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
-----  
EMBL; L41939; AAA99310.1; -;  
EMBL; D31661; BAA06506.1; -;  
EMBL; AF025304; AAB94602.1; -;  
EMBL; D14717; BAA03537.1; -;  
EMBL; L36643; AAB74244.1; -;  
EMBL; D37827; BAA07073.1; -;  
EMBL; X59292; CAA41981.1; -;  
PIR; A57174; A57174.  
PDB; 1B4F; X-ray; A/B/C/D/E/F/G/H=-.  
PDB; 1F0N; X-ray; A=905-986.  
Genew; HGNC:3393; EPHB2.  
MIM; 600997; -;  
GO; GO:0016021; C:integral to membrane; TAS.  
GO; GO:0005005; P:transmembrane-ephrin receptor activity; TAS.  
GO; GO:0007399; P:neurogenesis; TAS.  
GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
InterPro; IPR006209; EGF like.  
InterPro; IPR001090; Ephrin receptor.  
InterPro; IPR003962; FNIII subd.  
InterPro; IPR003961; FNIII.  
InterPro; IPR008957; FN\_III-like.  
InterPro; IPR008979; Gal\_bind like.  
InterPro; IPR011009; Kinase like.  
InterPro; IPR007019; Prot kinase.  
InterPro; IPR001650; SAM.  
InterPro; IPR001245; Tyr\_kinase.  
InterPro; IPR008266; Tyr\_kinase\_AS.  
InterPro; IPR001426; YKase\_receptorV.  
Pfam; PF01404; Ephrin\_lbd; 1.  
Pfam; PF00041; fn3; 2.  
Pfam; PF00069; Pkinase; 1.  
Pfam; PF00536; SAM; 1.  
PRINTS; PR00014; FNTYPEIII.  
PRINTS; PR00109; TYRKINASE.  
ProDom; PD001495; Ephrin\_receptor; 1.  
ProDom; PD000001; Prot\_kinase; 1.  
SMART; SM00615; EPH\_lbd; 1.  
SMART; SM00060; FN3; 2.  
SMART; SM00454; SAM; 1.  
SMART; SM00219; TYRK; 1.  
PROSITE; PS01186; EGF\_2; 1.



RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
 CC receptor subfamily.  
 DR EMBL; BC043088; AA043088.1; -;  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR003962; FcIII subd.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR011009; Kinase-like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR011510; SAM 2.  
 DR InterPro; IPR010993; SAM\_homology.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008266; Tyr\_kinase\_AS.  
 DR Pfam; PF01404; Ephrin\_lbd; 1.  
 DR Pfam; PF00041; fn3\_2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00536; SAM\_1; 1.  
 DR Pfam; PF07647; SAM\_2; 1.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR ProDom; PD00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00615; EPH\_lbd; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; TyrcK; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS00853; FN3; 2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS00105; SAM\_DOMAIN; 1.  
 KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;  
 KW Transmembrane; Tyrosine-protein kinase.  
 FT NON\_TER 1

SQ SEQUENCE 1021 AA; 113271 MW; 2BA741083DEC6164 CRC64;  
 Query Match 99.6%; Score 5168; DB 2; Length 1021;  
 Best Local Similarity 99.4%; Pred. No. 2e-314; 1; Indels 0; Gaps 0;  
 Matches 980; Conservative 5; Mismatches 1;  
 QY 1 MALRRLLGALLLLPILAAVEETLMDSTTATAELIGMMVHPSPGWEEVSGYDENNTIRTYQ 60  
 DB 36 MAVRRLLGALLLLPILAAVEETLMDSTTATAELIGMMVHPSPGWEEVSGYDENNTIRTYQ 95  
 QY 61 VCNVFESSQNMLRTKPIRRRGARRIHVEMKFSVRDCSSIPSPVSGCKETFNLYYEADF 120  
 DB 96 VCNVFESSQNMLRTKPIRRRGARRIHVEMKFSVRDCSSIPSPVSGCKETFNLYYEADF 155  
 QY 121 DSATKTFPMNMPWVKVTIADDESFSQVDLGGVRVKNINTEVSRSGPVSRSFYLAQD 180  
 DB 156 DLATKTFPMNMPWVKVTIADDESFSQVDLGGVRVKNINTEVSRSGPVSRSFYLAQD 215  
 QY 181 YGCMSLIAVRVFRYKCPRIIONGAIFOETLSGAESTSLVAARGSCIANAEEDVDPKLY 240  
 DB 216 YGCMSLIAVRVFRYKCPRIIONGAIFOETLSGAESTSLVAARGSCIANAEEDVDPKLY 275  
 QY 241 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTGTFKANQGDCACTHCPINRRTTSEGA 300  
 DB 276 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTGTFKANQGDCACTHCPINRRTTSEGA 335  
 QY 301 TNCVCNGYVRADLDPLDMPCTTIPSAQAVISSVNETSILMLEWTPPDSGGREDLVYNI 360  
 DB 336 TNCVCNGYVRADLDPLDMPCTTIPSAQAVISSVNETSILMLEWTPPDSGGREDLVYNI 395  
 QY 361 ICKSCSGRGACTRCGDNVQYAPROQLGLTEPRIIYISDLAHTQYTFEIOAVNGVTDQSPF 420  
 DB 396 ICKSCSGRGACTRCGDNVQYAPROQLGLTEPRIIYISDLAHTQYTFEIOAVNGVTDQSPF 455  
 QY 421 SPOFASVNTTNOAAPSAVSIMHOVSRVDSITLSWSQDPQNGVILDYELQYKEELSE 480  
 DB 456 SPOFASVNTTNOAAPSAVSIMHOVSRVDSITLSWSQDPQNGVILDYELQYKEELSE 515  
 QY 481 YNATAIKSPNTVTVOGLKAGAIYVQVRARTVAGYGRYSGKMYFQMTAEAEQTSIOEK 540  
 DB 516 YNATAIKSPNTVTVOGLKAGAIYVQVRARTVAGYGRYSGKMYFQMTAEAEQTSIOEK 575  
 QY 541 LPLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600  
 DB 576 LPLIVGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 635  
 QY 601 TYEDPNEAVREPAKEIDISCVKIEQIVIGAGEFGEVCSGHLKLPCKREI FVAIKTKSGYT 660  
 DB 636 TYEDPNEAVREPAKEIDISCVKIEQIVIGAGEFGEVCSGHLKLPCKREI FVAIKTKSGYT 695  
 QY 661 EKORRDFLSEASIMGQFDHPNVTHLSEGVVTKSTPVMII TEFMENGSLDSFLRQNDGQTV 720  
 DB 696 EKORRDFLSEASIMGQFDHPNVTHLSEGVVTKSTPVMII TEFMENGSLDSFLRQNDGQTV 755  
 QY 721 IQLVGLMRLGIAAGMKYLADNMYVHRDLAARNILVNSNLVKCVSDFGLSRFLDDTSDPTY 780  
 DB 756 IQLVGLMRLGIAAGMKYLADNMYVHRDLAARNILVNSNLVKCVSDFGLSRFLDDTSDPTY 815  
 QY 781 TSALGGKIPIRWTAPAEAIQYRKFTSADVMSYGI VVMWEVMSYGERPYWMTNODVINAIE 840  
 DB 816 TSALGGKIPIRWTAPAEAIQYRKFTSADVMSYGI VVMWEVMSYGERPYWMTNODVINAIE 875  
 QY 841 QDYRLPPMDPCPSALHQLMLDCWQDRNHRPKFGQLVNTLDKMRNPNSLKAMAPLSSGI 900  
 DB 876 QDYRLPPMDPCPSALHQLMLDCWQDRNHRPKFGQLVNTLDKMRNPNSLKAMAPLSSGI 935  
 QY 901 NLPFLDRTIPDYTSFNTVDWELEAIKMGQYKESFANAGFTSFVDVQSMMMEDILRLGVTL 960  
 DB 936 NLPFLDRTIPDYTSFNTVDWELEAIKMGQYKESFANAGFTSFVDVQSMMMEDILRLGVTL 995  
 QY 961 AGHQKILNSIQVMRAQMNIQSVEV 986  
 DB 996 AGHQKILNSIQVMRAQMNIQSVEV 1021

RESULT 3  
Q6P5F1 PRELIMINARY; PRT; 1029 AA.  
AC Q6P5F1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Ephb2 protein (Fragment).  
GN Name=Ephb2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Whiting M., Madan A., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
CC receptor subfamily.  
DR EMBL; BC062924; AAH62924.1; .  
DR GO; GO:0008046; P:axon guidance receptor activity; IDA.  
DR GO; GO:0005003; F:ephrin receptor activity; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0005102; F:receptor binding; IDA.  
DR GO; GO:0007411; P:axon guidance; IDA.  
DR GO; GO:0007612; P:learning; IMP.  
DR GO; GO:0048170; P:positive regulation of long-term neuronal s...; IMP.  
DR GO; GO:0048168; P:regulation of neuronal synaptic plasticity; IMP.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR001090; Ephrin receptor.  
DR InterPro; IPR003962; FNIII subd.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR008979; Gal\_bind-like.  
DR InterPro; IPR011009; Kinase-like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001660; SAM.  
DR InterPro; IPR011510; SAM\_2.  
DR InterPro; IPR010993; SAM\_homology.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR InterPro; IPR008266; Tyr\_pkinase AS.  
DR InterPro; IPR001426; Ykase\_receptorV.

DR Pfam; PF01404; Ephrin\_lbd; 1.  
DR Pfam; PF00041; fn3; 2.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00536; SAM\_1; 1.  
DR Pfam; PF07647; SAM\_2; 1.  
DR PRINTS; PR00014; FNTYPEIIII.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD001495; Ephrin\_receptor; 1.  
DR ProDom; PD000001; prot\_kinase; 1.  
DR SMART; SM00615; EPH\_lbd; 1.  
DR SMART; SM00060; FN3; 2.  
DR SMART; SM00454; SAM; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS00853; FN3\_2.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR PROSITE; PS0105; SAM\_DOMAIN; 1.  
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;  
KW transferase; Transmembrane; Tyrosine-protein kinase.  
FT NON\_TER 1  
SQ SEQUENCE 1029 AA; 114282 MW; A920A28E4A9A93BA CRC64;  
Query Match 99.4%; Score 5157.5; DB 2; Length 1029;  
Best Local Similarity 99.3%; Pred. No. 9e-314;  
Matches 980; Conservative 5; Mismatches 1; Indels 1; Gaps 1;  
QY 1 MALRLRGAALLLLPLLAAVEETLMDSTTATAELGWMVHPSPSGWEEVSGYDENNTIRTYQ 60  
DB 43 MAVRLRGAALLLLPLLAAVEETLMDSTTATAELGWMVHPSPSGWEEVSGYDENNTIRTYQ 102  
QY 61 VCNVFESSQNWLRTKFIIRRGGAHRIHVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADF 120  
DB 103 VCNVFESSQNWLRTKFIIRRGGAHRIHVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADF 162  
QY 121 DSATKTFNNMNPWKVDTIADSFQVDLGRVKNKINTEVRSFGPVSRSGFYLAQD 180  
DB 163 DLATKTFNNMNPWKVDTIADSFQVDLGRVKNKINTEVRSFGPVSRSGFYLAQD 222  
QY 181 YGCMSLIAVRVYRKPRIIQAALFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
DB 223 YGCMSLIAVRVYRKPRIIQAALFQETLSGAESTSLVAARGSCIANAEVDVPIKLY 282  
QY 241 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTFKANQGDCACTHCPINRSTTSEGA 300  
DB 283 CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSTFKANQGDCACTHCPINRSTTSEGA 342  
QY 301 TNCVCRNGYRADLDFLDMPTCTIPAPQAVISSVNETSLMLEWTPPRDSGGREDLYVNI 360  
DB 343 TNCVCRNGYRADLDFLDMPTCTIPAPQAVISSVNETSLMLEWTPPRDSGGREDLYVNI 402  
QY 361 ICKSCSGRGACTRCGDNVQVAPROGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPF 420  
DB 403 ICKSCSGRGACTRCGDNVQVAPROGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPF 462  
QY 421 SPQFASVNIITNOAAPSVAISMHVSRVDSITLSWSQDPQNGVILDYELQYKEL-ELS 479  
DB 463 SPQFASVNIITNOAAPSVAISMHVSRVDSITLSWSQDPQNGVILDYELQYKEL-ELS 522  
QY 480 EYNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGYGRYSGMYQFTWTEAEYQTSIQE 539  
DB 523 EYNATAIKSPTNTVTVOGLKAGAIYVQVARTVAGYGRYSGMYQFTWTEAEYQTSIQE 582  
QY 540 KLPLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHMTGPKMGIYDP 599  
DB 583 KLPLIIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHMTGPKMGIYDP 642  
QY 600 FTYEDPNEAVREFAKSIDISCVKIEQVIGAGEFGEVCSGHLKLPKGRIFVAIKLKSgy 659

Db 643 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGY 702  
QY  
Db 660 TEKORRDFLSEASIMGQFDHPNVHLEGVVTKSTPVMIIITEFMENGSLDSFLQNDGQFT 719  
QY  
Db 703 TEKORRDFLSEASIMGQFDHPNVHLEGVVTKSTPVMIIITEFMENGSLDSFLQNDGQFT 762  
QY  
Db 720 VIQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLDDTSDPT 779  
Db 763 VIQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLDDTSDPT 822  
QY  
Db 780 YTSALGKGKIPIRWTAPPAIQYRKFTSASDVWSYGIWVMEVMSYGERPYMDMTQDVINAI 839  
Db 823 YTSALGKGKIPIRWTAPPAIQYRKFTSASDVWSYGIWVMEVMSYGERPYMDMTQDVINAI 882  
QY  
Db 840 EODYRLPPPPMDCPSALHQLMDCWKDRNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 899  
Db 883 EODYRLPPPPMDCPSALHQLMDCWKDRNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 942  
QY  
Db 900 INPLPDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMEDILRLGVT 959  
Db 943 INPLPDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMEDILRLGVT 1002  
QY  
Db 960 LAGHOKILNSIQVMRAQMNQIQSVEV 986  
Db 1003 LAGHOKILNSIQVMRAQMNQIQSVEV 1029  
RESULT 4  
AAH62924 PRELIMINARY; PRT; 1029 AA.  
ID AAH62924  
AC AAH62924;  
DC 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Ephb2 protein (Fragment).  
GN EPHB2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC062924; AAH62924.1; -;  
FT NON TER 1  
SQ SEQUENCE 1029 AA; 114282 MW; A920A28E4A9A93BA CRC64;

Query Match 99.4%; Score 5157.5; DB 2; Length 1029;  
Best Local Similarity 99.3%; Pred. No. 9e-314;  
Matches 980; Conservative 5; Mismatches 1; Indels 1; Gaps 1;  
QY 1 MALRRLLGAALLLLPILAAVEETLMDSTTAAELGVMVHPSPSGWEEYSGVDENNTIRTYQ 60  
Db 43 MAVRRLLGAALLLLPILAAVEETLMDSTTAAELGVMVHPSPSGWEEYSGVDENNTIRTYQ 102  
QY 61 VCNVFESSQNNMLRTKFIERRGAHRHIVEMKESVRDCSSIPSPSGCKETFNLYYEADF 120  
Db 103 VCNVFESSQNNMLRTKFIERRGAHRHIVEMKESVRDCSSIPSPSGCKETFNLYYEADF 162  
QY 121 DSATKTFPNMNPWKVDTIAADESFQVDLGGRVKMKINTEVRSFGPVSRSFYLAQD 180  
Db 163 DLATKTFPNMNPWKVDTIAADESFQVDLGGRVKMKINTEVRSFGPVSRSFYLAQD 222  
QY 181 YGCGMSLIAVRVYRCPRIIQNGAIFOETLSAESTSLVAARGSCIANAEVDVPIKLY 240  
Db 223 YGCGMSLIAVRVYRCPRIIQNGAIFOETLSAESTSLVAARGSCIANAEVDVPIKLY 282  
QY 241 CNGDGEWLVPIGRCMCKAGFEAVENGTCVRCGCPSTGTFKANQGDCACTHCPINSRTTSEGA 300  
Db 283 CNGDGEWLVPIGRCMCKAGFEAVENGTCVRCGCPSTGTFKANQGDCACTHCPINSRTTSEGA 342  
QY 301 TNCVCRNGYRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRSGGREDLVYNI 360  
Db 343 TNCVCRNGYRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRSGGREDLVYNI 402  
QY 361 ICKSCGSGRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGVTPQSPF 420  
Db 403 ICKSCGSGRGACTRCGDNVQYAPROGLTEPRIYISDLAHTQYTFEIOAVNGVTPQSPF 462  
QY 421 SPOFASVNTTNOAAPSAVSIMHQVSRVTDSITLSWSQDPQPNQNGVILDYELQYEEK-ELS 479  
Db 463 SPOFASVNTTNOAAPSAVSIMHQVSRVTDSITLSWSQDPQPNQNGVILDYELQYEEKELS 522  
QY 480 EYNATAIKPTNTVTVOGLKAGAIYVQVRARTVAGYGRYSGWYFQTMTEABYQISIQE 539  
Db 523 EYNATAIKPTNTVTVOGLKAGAIYVQVRARTVAGYGRYSGWYFQTMTEABYQISIKE 582  
QY 540 KLPLIIGSSAAGLFLIAVVTVAIVCNRRGFRADSEYTDKLOHTSGHMTGPKMKIYIDP 599  
Db 583 KLPLIIGSSAAGLFLIAVVTVAIVCNRRGFRADSEYTDKLOHTSGHMTGPKMKIYIDP 642  
QY 600 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGY 659  
Db 643 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTLKSGY 702  
QY 660 TEKORRDFLSEASIMGQFDHPNVHLEGVVTKSTPVMIIITEFMENGSLDSFLQNDGQFT 719  
Db 703 TEKORRDFLSEASIMGQFDHPNVHLEGVVTKSTPVMIIITEFMENGSLDSFLQNDGQFT 762  
QY 720 VIQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLDDTSDPT 779  
Db 763 VIQLVGMRLGIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLDDTSDPT 822  
QY 780 YTSALGKGKIPIRWTAPPAIQYRKFTSASDVWSYGIWVMEVMSYGERPYMDMTQDVINAI 839  
Db 823 YTSALGKGKIPIRWTAPPAIQYRKFTSASDVWSYGIWVMEVMSYGERPYMDMTQDVINAI 882  
QY 840 EODYRLPPPPMDCPSALHQLMDCWKDRNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 899  
Db 883 EODYRLPPPPMDCPSALHQLMDCWKDRNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 942  
QY 900 INPLPDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMEDILRLGVT 959  
Db 943 INPLPDRTPIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMEDILRLGVT 1002  
QY 960 LAGHOKILNSIQVMRAQMNQIQSVEV 986  
Db 1003 LAGHOKILNSIQVMRAQMNQIQSVEV 1029









```

Db 911 MAPSSGWNPLLDRTIPDYTSFNTVDWLDAIKMSQYKESFASAGFTTFDIIVSQMTVED 970
Qy 953 ILRLGVTLAGHOKKILNSIQVMRAQMNQIOSVEV 986
Db 971 ILRVLGVTLAGHOKKILNSIQVMRAQMNQIOSVEV 1004

RESULT 7
EPB3_COTJA
ID EPB2_COTJA STANDARD; PRT; 987 AA.
AC Q90344;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor QK5).
GN Name=EPHB2; Synonyms=QK5;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Kenny D., Bronner-Frazer M., Marcelle C.;
RT "the receptor tyrosine kinase QK5 mRNA is expressed in a gradient
RL Dev. Biol. 172:708-716(1995).
CC -!- FUNCTION: Receptor for members of the ephrin-B family.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the tyr family of protein kinases. Ephrin
CC receptor subfamily.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; X91737; CAA62862.1; -.
CC HSP; P54763; IJPA.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR001090; Ephrin receptor.
CC InterPro; IPR003962; FNIII subd.
CC InterPro; IPR003961; FNIII.
CC InterPro; IPR008979; FN III-like.
CC InterPro; IPR008979; Gal bind like.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR001660; SAM.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR008266; Tyr_kinase_AS.
CC InterPro; IPR001426; YKase receptorV.
CC Pfam; PF01404; Ephrin_lbd; 1.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00536; SAM; 1.
CC PRINTS; PR00014; FNYPEIII.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD001495; Ephrin_receptor; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00615; EPH_lbd; 1.
CC SMART; SM00060; FN3_2.
CC SMART; SM00454; SAM; 1.
CC SMART; SM00219; TyRc; 1.

```

```

DR PROSITE; PS01186; EGF 2; UNKNOWN_1.
DR PROSITE; PS05853; FN3; 2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; FALSE_NEG.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS0105; SAM DOMAIN; 1.
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
KW transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 987 Ephrin type-B receptor 2.
FT DOMAIN 20 544 Extracellular (Potential).
FT TRANSMEM 545 565 Potential.
FT DOMAIN 566 987 Cytoplasmic (Potential).
FT DOMAIN 185 322 Cys-rich.
FT DOMAIN 323 427 Fibronectin type-III 1.
FT DOMAIN 428 528 Fibronectin type-III 2.
FT DOMAIN 622 885 Protein kinase.
FT DOMAIN 914 978 SAM.
FT SITE 985 987 PDZ-binding motif (Potential).
FT NP_BIND 628 636 ATP (By similarity).
FT BINDING 654 654 ATP (By similarity).
FT ACT_SITE 747 747 Phosphotyrosine (by autocatalysis)
FT MOD_RES 597 597 (Potential).
FT MOD_RES 603 603 Phosphotyrosine (by autocatalysis)
FT MOD_RES 781 781 (Potential).
FT MOD_RES 931 931 Phosphotyrosine (by autocatalysis)
FT CARBOHYD 266 266 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 337 337 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 429 429 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 478 478 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 483 483 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 987 AA; 110331 MW; 05D6EC68E718DD7 CRC64;

Query Match 95.3%; Score 4945; DB 1; Length 987;
Best Local Similarity 94.9%; Pred. No. 1.7e-300; Indels 0; Gaps 0;
Matches 927; Conservative 30; Mismatches 20;

Qy 10 LLLPLLAAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQ 69
Db 11 LALLPLLAAVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQ 70
Qy 70 NNWLRTKPIRRRGARHIVEMKESVDCCSIPSPGSCKETFNLYYYEADFDSATKTPN 129
Db 71 NNWLRTKPIRRRGARHIVEMKESVDRDCSSIPNVPGSCKETFNLYYYESDFDSATKTPN 130
Qy 130 WMENPWVKVDITAADESFSQVDLGGVWKINTVRSFGVPSRSGFYLAFOYGGCMSLIA 189
Db 131 WMENPWVKVDITAADEFSDVLGGVWKINTVRSFGVPSRSGFYLAFOYGGCMSLIA 190
Qy 190 VRVYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 249
Db 191 VRVYRKCPRIIQNGADFQETLSGAESTSLVASRGTCINKAEVDVPIKQHCNGDGEWLV 250
Qy 250 PIGRCMKAGFAVENGTVCRCGPGSTFKANOGDEACTHCPINSTRTSSGATNCVCRNGY 309
Db 251 PIGRCMKRPGYESVANGTVCRCGPGSTFKASQSGDEGCVHCPIINSTRTSSGATNCVCRNGY 310
Qy 310 YRADLDPDMPCTTIPSAQVAVISSVNETSLMLEWTPPRDSDGGRDLVYNIICKSCGSGR 369
Db 311 YRADLDPDMPCTTIPSAQVAVISSVNETSLMLEWTPPRDSDGGRDLVYNIICKSCGSGR 370
Qy 370 GACTRCGDNVQYAPROGLTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSPQFASVNI 429
Db 371 GACTRCGDNVQYAPROGLTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSPQFASVNI 430
Qy 430 TTNQAAPSAVSIMHOVSRVTDSITLWSQDPQNGVILDYELQYKEKELSEYNATAIKSP 489

```

Db 431 TTNQAPSAVSIMHQVSRVDSITLSWSPQDPQNGVILDVYELQYKKNLSNLTAVKSP 490  
Qy 490 TINTVVOGLKAGAIYVFQVARTVAGYGRYSGKMYFQMTTEAEYQTSIQEKLPLIGSSA 549  
Db 491 TINTVVOGLKAGAIYVFQVARTVAGYGRYSGKMYFQMTTEAEYQTSIQEKLPLIGSSA 550  
Qy 550 AGLVFLAVVIAVNCRRGPERADSEYTDKLOHYTSGHMTGPKKIYIDPFTYEDPNEAV 609  
Db 551 AGLVFLAVVIAVNCRRGPERADSEYTDKLOHYTSGHMTGPKKIYIDPFTYEDPNEAV 610  
Qy 610 REPAKEIDISCVEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGVTEKORRDFLS 669  
Db 611 REPAKEIDISCVEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGVTEKORRDFLS 670  
Qy 670 EASIMGQFDHPNVILHLEGVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVIQVGLMLRG 729  
Db 671 EASIMGQFDHPNVILHLEGVTKSTPVMIIITEFMENGLSDSFLRQNDGQFTVIQVGLMLRG 730  
Qy 730 IAAGMKYLADNMYVHRDLAARNILVNSNLVKCVSDFGLSRFLDDTSDPTYSALGCKIP 789  
Db 731 IAAGMKYLADNMYVHRDLAARNILVNSNLVKCVSDFGLSRFLDDTSDPTYSALGCKIP 790  
Qy 790 IRWTAPAIQYRKFTSADVMSYGVIMVWVMSYGERPYWDMTNQDVINAIEQDYRLPPLPM 849  
Db 791 IRWTAPAIQYRKFTSADVMSYGVIMVWVMSYGERPYWDMTNQDVINAIEQDYRLPPLPM 850  
Qy 850 DCPALHQLMDCQKQDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGNLPLLDRTI 909  
Db 851 DCPALHQLMDCQKQDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGNLPLLDRTI 910  
Qy 910 PDYTSFNTVDEWLBAIKMGQYKESFANAGTSPFVQVMSQMMEDILRLGVTLGHQKKILN 969  
Db 911 PDYTSFNTVDEWLBAIKMGQYKESFANAGTSPFVQVMSQMMEDILRLGVTLGHQKKILN 970  
Qy 970 SIQVRAQMNQIQSVEV 986  
Db 971 SIQVRAQMNQIQSVEV 987

RESULT 8  
EPB1\_RAT  
ID EPB1\_RAT STANDARD; PRT; 984 AA.  
AC P09759;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ephrin type-B receptor 1 precursor (EC 2.7.1.112) (Tyrosine-protein  
kinase receptor Eph-2) (ELK).  
GN Name=EphB1; Synonyms=Eph2, Elk;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wistar; TISSUE=Brain;  
RX MEDLINE=91203869; PubMed=2017163;  
RA Lhotak V., Greer P., Letwin K., Pawson T.;  
RT "Characterization of elk, a brain-specific receptor tyrosine kinase.";  
RL Mol. Cell. Biol. 11:2496-2502(1991).  
RN [2]  
RP SEQUENCE OF 605-984 FROM N.A.  
RC STRAIN=Wistar; TISSUE=Brain;  
RX MEDLINE=94167102; PubMed=2485255;  
RA Letwin K., Yee S.P., Pawson T.;  
RT "Novel protein-tyrosine kinase cDNAs related to fps/fes and eph cloned  
using anti-phosphotyrosine antibody.";  
RL Oncogene 3:621-627(1988).  
CC -1- FUNCTION: Receptor for members of the ephrin-B family. Binds to  
ephrin-B1, -B2 and -B3. May be involved in cell-cell interactions  
in the nervous system.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
tyrosine phosphate.

CC -1- SUBUNIT: The ligand-activated form interacts with GRB2, GRB10 and  
NCK through their respective SH2 domains. The GRB10 SH2 domain  
binds EPHB1 through Tyr-928, while GRB2 binds residues within the  
catalytic domain. The NCK SH2 domain binds EPHB1 through Tyr-594.  
CC Interacts with PRKABP (By similarity).  
CC SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Restricted to brain and testes.  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
receptor subfamily.  
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/annouce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M59814; -; NOT ANNOTATED\_CDS.  
CC EMBL; X13411; CAA31777.1; -;  
CC PIR; A39753; A39753.  
CC HSP; P54763; J3PA.  
CC InterPro; IPR006209; EGF like.  
CC InterPro; IPR001090; Ephrin receptor.  
CC InterPro; IPR003962; FniIII subd.  
CC InterPro; IPR003961; FN III.  
CC InterPro; IPR008957; FN-III-like.  
CC InterPro; IPR008979; Gal\_bind-like.  
CC InterPro; IPR011009; Kinase like.  
CC InterPro; IPR000719; Prot\_kinase.  
CC InterPro; IPR001660; SAM.  
CC InterPro; IPR001245; Tyr\_kinase.  
CC InterPro; IPR008266; Tyr\_kinase\_AS.  
CC InterPro; IPR001426; YKase\_receptorV.  
CC Pfam; PF01404; Ephrin\_lbd; 1.  
CC Pfam; PF00041; fn3; 2.  
CC Pfam; PF00069; Pkinase; 1.  
CC Pfam; PF00536; SAM; 1.  
CC PRINTS; PR00014; FNTYPEIII.  
CC PRINTS; PR00109; TYRKINASE.  
CC ProDom; PD001495; Ephrin\_receptor; 1.  
CC ProDom; PD000001; Prot\_kinase; 1.  
CC SMART; SM00615; EPH\_lbd; 1.  
CC SMART; SM00060; FN3; 2.  
CC SMART; SM00454; SAM; 1.  
CC SMART; SM00219; TyRK; 1.  
CC PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
CC PROSITE; PS00853; FN3; 2.  
CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
CC PROSITE; PS00107; PROTEIN\_KINASE\_DOM; 1.  
CC PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
CC PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
CC PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
CC PROSITE; PS0105; SAM\_DOMAIN; 1.  
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;  
KW Transferase; Transmembrane; Tyrosine-protein kinase.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 984 Ephrin type-B receptor 1.  
FT DOMAIN 18 540 Extracellular (Potential).  
FT TRANSMEM 541 563 Potential.  
FT DOMAIN 564 984 Cytoplasmic (Potential).  
FT DOMAIN 183 319 Cys-rich.  
FT DOMAIN 323 424 Fibronectin type-III 1.  
FT DOMAIN 430 525 Fibronectin type-III 2.  
FT DOMAIN 619 882 Protein kinase.  
FT DOMAIN 911 975 SAM.  
FT SITE 982 984 PDZ-binding motif (Potential).  
FT NP\_BIND 625 633 ATP (By similarity).  
FT BINDING 651 651 ATP (By similarity).  
FT ACT\_SITE 744 744 By similarity.  
FT MOD\_RES 594 594 Phosphotyrosine (by autocatalysis)

```
FT MOD_RES 600 600 (Potential).
FT Phosphotyrosine (by autocatalysis)
FT MOD_RES 778 778 (Potential).
FT Phosphotyrosine (by autocatalysis)
FT MOD_RES 928 928 (Potential).
FT Phosphotyrosine (by autocatalysis)
FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 426 426 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 480 480 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 984 AA; 109882 MW; 521EAC240D8F91A CRC64;

Query Match
Best Local Similarity 75.8%; Score 3934.5; DB 1; Length 984;
Matches 720; Conservative 128; Mismatches 125; Indels 1; Gaps 1;

QY 11 LLLPLLAETLMDSTTAELGMMVHPHSGWEEVSGYDENNTTIRTVQVNCNVPSSQN 70
Db 10 LLASAVAAMEETLMDTRTAAELGWTANPASGWEEVSGYDENLNTIRTVQVNCNVPNQ 69
QY 71 NWLRTKFIIRRGARHIVENKFSVRDCSSITPSVPGCKETFNLYYYEADFSATKTFPNW 130
Db 70 NWLTLTFINRGARHIVETMRFTVRDCSSLPNVPGCKETFNLYYYETSDVIATKKSAFW 129
QY 131 MENPFWKVDITAADESPQVDLGRVMKINTEVRSFGPVSRSRFGYLAQDYGCMSLIIV 190
Db 130 SEAPYLKVDITAADESPQVDLGRVMKINTEVRSFGPVSRSRFGYLAQDYGCMSLIIV 189
QY 191 RVFYRKPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGBWLVP 250
Db 190 RVFFFKCPSIQVNFVAVPTMTGAESTSLVARGTCIPNAEVDVPIKLYCNGDGBWMP 249
QY 251 IGRMCKAGFAENVGTVCGCSGTFKANOGBEACHCPINSTRTSEGATNCVCRNGY 310
Db 250 IGRCTCKAGYEP-ENSVACACACAGTFCASQEAEGCSHCPSNSRSPSEASPICTCTG 308
QY 311 RADLDPLDMPCTTIPSAPOAVISVNETSLMLEWTPDRDSCGRDLYNIIICKSCSGRG 370
Db 309 RADFDPEVACTSVPSGPRNIVSIVNETSIILWHHPRETGGDDVTYNIICKCRADR 368
QY 371 ACTRCGDNVOYARQLGLTEPRIYISDLAHTQYTFEIQAVNGVTPOSPSPFASVNIT 430
Db 369 SCRCDDNVEFVRQLGLTECRVSISSLAHTPYTFDQIAINGVSSKSPPPQHVSNIT 428
QY 431 TNQAPASAVSMHQVSTVDITLSQSDOPNGVLDVLOYEYKELSEYNATATKSP 490
Db 429 TNQAPASTVPMHQVSTVDITLSQSDOPNGVLDVLOYEYKELSEYNATATKSP 488
QY 491 NTVTVQGLKAGAIYVFOVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSAA 550
Db 489 NTAIDGLRPGMYVVOVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIIGSAA 548
QY 551 GLVPLIAVVAIVCNRRGFERADSEYTDKLOHYTSGHMTPGKMIYIDPTTYEDPNEVR 610
Db 549 GWVFWSLVAISVCSRKAYSKEAVYSDKLOHYTSGRSGPMKIYIDPTTYEDPNEVR 608
QY 611 EFAKEIDISCKVLEOVIGAGEFCVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSE 670
Db 609 EFAKEIDVSVFKIEVIGAGEFGVYGRULKPKREIYVAIKTLKAGYSEKORRDLSE 668
QY 671 ASIMGQFDHPNVHLEGVVTWKTSPVMIITBFMENGSLDSFLRQNDGQFTVIQVGLMRLGI 730
Db 669 ASIMGQFDHPNITFLEGVVTWKTSPVMIITBFMENGSLDSFLRQNDGQFTVIQVGLMRLGI 728
QY 731 AAGMKYLADNMYVHRDLAARNILVNSLVCKVSDPGLSRFLEDTSPTTYSALGGKIP 790
Db 729 AAGMKYLSEMYVHRDLAARNILVNSLVCKVSDPGLSRFLEDTSPTTYSALGGKIP 788
QY 791 RWTAPAEIQRKFTSASDVMSYGIYVMEVMSYGERPVDWNTDQVINAISQDYLPPMD 850
Db 789 RWTAPAEIQRKFTSASDVMSYGIYVMEVMSYGERPVDWNTDQVINAISQDYLPPMD 848
QY 851 CPSALHQLMLDCWQKDRNRPKFGQIVNTLDKMIARNPNSLKAMAPLSSGINPLDRTIP 910
```

```
Db 849 CPAALHQLMLDCWQKDRNRPKFAEIVNTLDKMIARNPNSLKATVATVPSQPLDRSIP 908
QY 911 DYTSTFVTVDEWLEAKMGQYKESFANAGTSDVVSQMMEDILRLGVTLGAGHOKILNS 970
Db 909 DFTAFVTVDDWLSAIKMWQYRDSFLTAGFTSLQVLTQMTSDBLLRIGVTLGAGHOKILNS 968
QY 971 IQVMRAQMNQIOISV 984
Db 969 IHSMRVQMNQSPSV 982

RESULT 9
Q8CBF3 PRELIMINARY: PRT; 984 AA.
AC Q8CBF3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:9630041E07 product:Eph receptor B1, full
DE insert sequence.
GN Name=EphA1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akizawa J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
```





OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Fetal brain;  
 RX MEDLINE=96115594; PubMed=8666391;  
 RA Tang X.X., Biegel J.A., Nycum L.M., Yoshioka A., Brodeur G.M.,  
 RA Pleasure D.E., Ikegaki N.;  
 RT "cDNA cloning, molecular characterization, and chromosomal  
 RT localization of NET(EPH2), a human EPH-related receptor protein-  
 RT tyrosine kinase gene preferentially expressed in brain.";  
 RL Genomics 29:426-437(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).  
 RC TISSUE=Kidney;  
 RA Stein E., Schoecklmann H.O., Daniel T.O.;  
 RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 18-32.  
 RA Zhang Z., Henzel W.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites.";  
 RL Submitted (JUN-2004) to Swiss-Prot.  
 RN [4]  
 RP INTERACTIONS WITH GRB2 AND GRB10.  
 RX MEDLINE=96394464; PubMed=8798570;  
 RA Stein E., Cerretti D.P., Daniel T.O.;  
 RT "Ligand activation of ELK receptor tyrosine kinase promotes its  
 RT association with Grb10 and Grb2 in vascular endothelial cells.";  
 RL J. Biol. Chem. 271:23588-23593(1996).  
 CC [1]- FUNCTION: Receptor for members of the ephrin-B family. Binds to  
 CC ephrin-B1, -B2 and -B3. May be involved in cell-cell interactions  
 CC in the nervous system.  
 CC [2]- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC [3]- SUBUNIT: The ligand-activated form interacts with GRB2, GRB10 and  
 CC NCK through their respective SH2 domains. The GRB10 SH2 domain  
 CC binds EPHB1 through Tyr-928, while GRB2 binds residues within the  
 CC catalytic domain. The NCK SH2 domain binds EPHB1 through Tyr-594.  
 CC Interacts with PRKCAP (By similarity).  
 CC [4]- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC [5]- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=EPHB1A;  
 CC IsoId=P54762-1; Sequence=Displayed;  
 CC Name=2; Synonyms=EPHB1B;  
 CC IsoId=P54762-2; Sequence=VSP\_003013;  
 CC Name=3; Synonyms=EPHB1C;  
 CC IsoId=P54762-3; Sequence=VSP\_003015;  
 CC Name=4; Synonyms=EPHB1D;  
 CC IsoId=P54762-4; Sequence=VSP\_003014;  
 CC [6]- TISSUE SPECIFICITY: Preferentially expressed in brain.  
 CC [7]- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
 CC receptor subfamily.  
 CC [8]- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC [9]- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
 CC -----  
 CC EMBL; L40636; AAB08520.1; -;  
 CC EMBL; AF037331; AAD02030.1; -;  
 CC EMBL; AF037332; AAD02031.1; -;  
 CC EMBL; AF037333; AAB94627.1; -;  
 CC EMBL; AF037334; AAB94628.1; -;  
 CC HSSP; P54763; 1JPA.  
 CC InAct; P54762; -;

DR Genew; HGNC:3392; EPHB1.  
 DR MIM; 606000; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS.  
 DR GO; GO:0007399; P:neurogenesis; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR003962; FNIII\_subd.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR InterPro; IPR001426; YKase\_receptorV.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00536; Pkinase; 1.  
 DR PRINTS; PR00014; ENTPEIIL.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00615; EPH\_lbd; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; TyTKC; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS00853; FN3; 2.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TVR; 1.  
 DR PROSITE; PS00109; RECEPTOR\_TVR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TVR\_KIN\_V\_2; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TVR\_KIN\_V\_2; 1.  
 DR PROSITE; PS00105; SAM\_DOMAIN; 1.  
 KW Alternative splicing; ATP-binding; Direct protein sequencing;  
 KW Glycoprotein; Phosphorylation; Polymorphism; Receptor; Repeat; Signal;  
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.  
 FT SIGNAL 1 17  
 FT CHAIN 18 984 Ephrin type-B receptor 1.  
 FT DOMAIN 18 540 Extracellular (Potential).  
 FT TRANSMEM 541 563 Potential.  
 FT DOMAIN 564 984 Cytoplasmic.  
 FT DOMAIN 183 319 Cys-rich.  
 FT DOMAIN 323 424 Fibronectin type-III 1.  
 FT DOMAIN 430 525 Fibronectin type-III 2.  
 FT DOMAIN 619 882 Protein kinase.  
 FT DOMAIN 911 975 SAM.  
 FT SITE 982 984 PDZ-binding motif (Potential).  
 FT NP\_BIND 625 633 ATP (By similarity).  
 FT BINDING 651 651 ATP (By similarity).  
 FT ACT\_SITE 744 744 By similarity.  
 FT MOD\_RES 594 594 Phosphotyrosine (by autocatalysis).  
 FT MOD\_RES 600 600 Phosphotyrosine (by autocatalysis) (Potential).  
 FT MOD\_RES 778 778 Phosphotyrosine (by autocatalysis) (Potential).  
 FT MOD\_RES 928 928 Phosphotyrosine (by autocatalysis).  
 FT CARBOHYD 334 334 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 426 426 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 480 480 N-linked (GlcNAc... ) (Potential).  
 FT VARSPPLIC 1 27 MALDYLLLLLLASAVAMEETLMDTTRT -> METREKKKSR  
 FT AERGTR (in isoform 2).  
 FT /FTId=VSP\_003013.  
 FT Missing (in isoform 4).  
 FT /FTId=VSP\_003014.  
 FT Missing (in isoform 3).  
 FT /FTId=VSP\_003015.  
 FT T -> S (in dbSNP:1042794).  
 FT /FTId=VAR\_011801.



FT VARIANT 152 152 G -> R (in dbSNP:1042793).  
/FTid=VAR\_011802.  
FT VARIANT 367 367 R -> G (in dbSNP:1042789).  
/FTid=VAR\_011803.  
FT VARIANT 485 485 R -> S (in dbSNP:1042788).  
/FTid=VAR\_011804.  
FT VARIANT 847 847 M -> T (in dbSNP:1042785).  
/FTid=VAR\_011805.  
FT CONFLICT 12 12 A -> E (in Ref. 2).  
FT CONFLICT 185 185 S -> I (in Ref. 2).  
FT CONFLICT 274 274 T -> R (in Ref. 2).  
FT CONFLICT 336 336 T -> S (in Ref. 2).  
FT CONFLICT 813 813 V -> H (in Ref. 2).  
FT CONFLICT 819 819 S -> Y (in Ref. 2).  
FT CONFLICT 973 973 R -> W (in Ref. 2).  
SQ SEQUENCE 984 AA; 109884 MW; 8044160824E93A92 CRC64;

Query Match 75.6%; Score 3924; DB 1; Length 984;  
Best Local Similarity 73.5%; Pred. No. 1.28-236;  
Matches 720; Conservative 130; Mismatches 128; Indels 2; Gaps 2;

Qy 1 MALRRLGAALLLLPALLAABESTLMDSTTATAEALGWMVHPSPGSEVSGYDENMTIITYQ 60  
Db 1 MALDYL-LLLLASAVAWEETLMDTRTATAEALGWTANPASCWEVSGYDENMTIITYQ 59

Qy 61 VCNVFPSONWLRTKFIIRRGAIHRIHVMKFSVRDCSSIPSPGSKCTFNLYYYEADF 120  
Db 60 VCNVFPQNNWLLTTFINRRGAHRIIVTEMTFTVRDCSSLNPNVPGSKCTFNLYYYETDS 119

Qy 121 DSATKTFPNMENPWKVDITAADESPQVDLGRVMKINTEVRSFGVSRSGYLAFOD 180  
Db 120 VIATKGAFAFSEAPYKVDITAADESPQVDLGRVMKINTEVRSFGVSRSGYLAFOD 179

Qy 181 YGGCMSLIIVAFVYRKPRIIIONGAIFOEITLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
Db 180 YGACMSLLSVAFVFKKCPESIVONFAVPEPTWTGAEISTLVARTCTIPNAEVDVPIKLY 239

Qy 241 CNGDGEWLVPITGRCMKACGFAVENGTVCRCPSGTTFKANGDREACTHCPINSRTTSEGA 300  
Db 240 CNGDGEWVPIGRCTCKPGYEP-ENS VACKACAPAGTFKASQAEAGCSHCPSNRSRPAES 298

Qy 301 TNCVCRGYYRADLDPLDMPCTTIPSAPOAVISSNETSLMLEWTPRDSGREDLVYNI 360  
Db 299 PICTCRGYYRADLDPPEVACTSPVSGPRNIVISITSLWPPRETGGRDDVTYNI 358

Qy 361 ICKSCGSGRGACTCGDNVQVAPQLGLTEPRIYISDLLAHTOYTFBIQAVNGVTDOSPF 420  
Db 359 ICKKCRADRRSCSDNNVEFVPLQLGLTECRVSISSLWHTPTFDIQAINGVSSKSPF 418

Qy 421 SPQFASVNTITNOAPSASVIMHQSRTVDSITLSWQDQPNQGVILDYELQYKEKELSE 480  
Db 419 PPQHVSVNITITNOAPSSTVPIHQVSATMRISITLSWQPEQNGIILDYELQYKEKELSE 478

Qy 481 YNATAIKSPNTVTVOGLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEAYTSIOEK 540  
Db 479 FNSSMARSTNTARIDGLPGMVVQVQVARTVAGYKFGSKMCFQTLDDYKSELREQ 538

Qy 541 LPLIIGSAGLVFLIAVWVIAVCNRRGPRADSEYTDKLOHTYSGHMTPGMKIYIDPF 600  
Db 539 LPLIAGSAGLVFVSVLVAISIVCSRKRAYSKAVYSDKLOHSTGRGSGFMKIYIDPF 598

Qy 601 TYEDPNEAVREFAKEIDISCVKIBQVIGAGBFVCSGHLKLPKGRIFVAIKTLKSGYT 660  
Db 599 TYEDPNEAVREFAKEIDVSVKIBEVIGAGBFVCSGHLKLPKGRIFVAIKTLKAGYS 658

Qy 661 EKQRDFLSEASINGQFDHPNVIHLEGVVTKSTPVMITFEMNGSLDSFLRQNDGQFTV 720  
Db 659 EKQRDFLSEASINGQFDHPNIIILEGVVTKSRPVMITFEMNGALDSFLRQNDGQFTV 718

Qy 721 IQLVGLRGLIAGMKYLADNMVVRDLAARNILVNSLVCKVSDFGLSRFLDDTSDPTY 780  
Db 719 IQLVGLRGLIAGMKYLAEMVVRDLAARNILVNSLVCKVSDFGLSRYLQDDTSDPTY 778

Qy 781 TSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGIWMVMSYGERPVDWMTNQDVINAIE 840  
Db 779 TSSLGKIPVWTAPEAIYRKFTSASDVMSYGIWMVMSYGERPVDWMTNQDVINAIE 838

Qy 841 QDYRLPPMDPCPSALHOLMDCWQKDRNHRPKFQIVNTLDMKIRNPNSLKAMAPLSSGI 900  
Db 839 QDYRLPPMDPCPALHOLMDCWQKDRNHRPKFQIVNTLDMKIRNPNSLKAMAPLSSGI 898

Qy 901 NLPLLDRTIPDYTSFNTVDEWLEAKMGQYKESFANAGFTSFVDVVSQMMEDIIRLGVTL 960  
Db 899 SQPLDRLSDIPDTAFTVDDWLSAIAKQVQYRDSFLTAGFTSLQLVQWTSDDLRLIGITL 958

Qy 961 AGHQKILNSIQVWRAQMNQ 980  
Db 959 AGHQKILNSIHSRMRVQISQ 978

RESULT 11  
Q6PG23 ID Q6PG23 PRELIMINARY; PRT; 984 AA.  
AC Q6PG23;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Eph receptor B1.  
GN Name=Ephb1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22398257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Stoenen C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.;  
Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
CC receptor subfamily.  
DR EMBL: BC057301; AAH57301.1; -;  
DR GO: GO:0005737; C:cytoplasm; IDA.  
DR GO: GO:0016020; C:membrane; IDA.  
DR GO: GO:0008046; F:axon guidance receptor activity; IDA.  
DR GO: GO:0007411; P:axon guidance; IDA.  
DR InterPro: IPR006209; EGF like.  
DR InterPro: IPR001090; Ephrin\_receptor.  
DR InterPro: IPR003962; FNIII\_subd.  
DR InterPro: IPR003961; FN\_III.



```
RP SEQUENCE FROM N.A.
RC STRAIN=CS5BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057301; AAH57301.1; -.
KW Receptor.
SQ SEQUENCE 984 AA; 109924 MW; 2E2F89942A8041A9 CRC64;

Query Match 75.5%; Score 3916.5; DB 2; Length 984;
Best Local Similarity 73.7%; Pred. No. 3.7e-236;
Matches 718; Conservative 127; Mismatches 128; Indels 1; Gaps 1;

QY 11 LLLPLLAVEETLMDSTTATLGLWVHPGSGWEVSGYDENMANTIRYQVNCVPESSON 70
DB 10 LLASAVAAMEETLMDTRTATLGLWNTANPASGEVSGYDENLNTIRYQVNCVPEPNQ 69
QY 71 NWLRTKFRRRGAHRIHVMKFSVRDCSSISPSVGSCKETFLNLYYADPDSATKTFPNW 130
DB 70 NWLLTFFINRGAHRIYTEMFTVRDCSSLNPNVGSCKETFLNLYYEDTSVIATKSAFW 129
QY 131 MENPMVKYDTTAADESPQVDLGGVRMKINTEVRSFGVSRSGFYLAQDYGCGMSLIAV 190
DB 130 SEAPYLKVDTTAADESPQVDLGGVRMKINTEVRSFGVSRSGFYLAQDYGCGMSLLSV 189
QY 191 RVFVKCPRIITONGAIFOTELSGABSTSLVAARSCIANABEVDPVILKYNCGOGEMLVP 250
DB 190 RVFFIKCPISIQNFAPVETWTGAESTSLVIARTGTCIPNABEVDVPIKLYCNGDGEWVP 249
QY 251 IGRWCCKAGFAVENVGTGRCPCSTKCANOGDEACTHCPINSTRTSEGATNCVCRNGY 310
DB 250 IGRCTCKPGYIP-ENSVACKAPAGTFKASQAEAGCSHCPSNSRSPSEAPICRTGY 308
QY 311 RADLDPLDMPCTTIPSAQVAIVSSVNETSLMLEWTPPRDSCGREDLVNIIICKSGSGRG 370
DB 309 RADPDPEVACTSPVSGPRNIVISVNETSIILEWHPPRETGDRDVTYNIICKRADRR 368
QY 371 ACTRCGNVQVAPQLGLTEPRIVISDLAHTQYTFEIQVANGVTDSPSPQFASVNIT 430
DB 369 SCSCDDNVEVPRLGLTECRVSTISSLWHTPTFTDQIAINGVSSKSPFPQHVSNIT 428
QY 431 TNOAPSASVIMHVSRTVDISITLSWQDOPNGVILDYELQYKEKELSEYNATAIKSPT 490
DB 429 TNOAPSIVPIHQVSATMRISITLSWQEPQNGIILDYELIYKEKEHNEFNFSMARST 488
QY 491 NTVTVQGLKAGAIYVQVARTVAGYGRYSKMTFQTMTEAYEYTSIQEKLPLIIGSSAA 550
DB 489 NTARIDGLRPGWVYVQVARTVAGYGRYSKMTFQTMTEAYEYTSIQEKLPLIIGSSAA 548
QY 551 GLVFLIAVVVIAVNCRRGPERADSEYTDKLOHTSGHMTGMIYIDPFTYEDPNEAVR 610
DB 549 GVWFVSLVAISIVCSRKRAYSKEAAYSQKLYSTGRSGPMKIYIDPFTYEDPNEAVR 608
QY 611 EFAKEIDISCVKIEQVIGAGFEGVCSGHLKLPKREIFVAIKTKSGYTEKORRDLSE 670
DB 609 EFAKEIDVSFKIEVIGAGFEGVGRKLPKREIYVAIKTKAGYSKQRDRDLSE 668
QY 671 ASIMGQDHPNVIHLEGVTKSTPMIITEFWENGSLDSFLRQNDGQFTVQLVGLMRLGI 730
DB 669 ASIMGQDHPNVIHLEGVTKSTPMIITEFWENGSLDSFLRQNDGQFTVQLVGLMRLGI 728
QY 731 AAGMKYLAQVYVHRDLAARNILNSNLVCKVDFGLSRFLEDDTSDPTYSALGGKIP 790
DB 729 AAGMKYLAQVYVHRDLAARNILNSNLVCKVDFGLSRFLEDDTSDPTYSALGGKIP 788
QY 791 RWTAPALQVKEFTSASDWSVSGYVMEVMSYGERPYWDMNQVINAIEDYELPPMD 850
DB 789 RWTAPALQVKEFTSASDWSVSGYVMEVMSYGERPYWDMNQVINAIEDYELPPMD 848
QY 851 CPSALHQLMDCWQKDRNRHFKFGQIVNTLDKMRNPNLSKAMAPLSSGINLPDLRTIP 910
DB 849 CPAALHQLMDCWQKDRNRHFKFGQIVNTLDKMRNPNLSKAMAPLSSGINLPDLRTIP 908
QY 911 DYTSTNTVDEWLEAIKMGQYKESFANAGTSTFVVSQMMMBDILRLGVTLAGHOKKILNS 970
```



DR HSP; P54763; LUPA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:000524; F:ATP binding; IEA.  
 DR GO; GO:0005003; F:ephrin receptor activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR001090; Ephrin receptor.  
 DR InterPro; IPR003962; FNIII subd.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR008979; Gal bind like.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR010993; SAM\_homology.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase AS.  
 DR InterPro; IPR001426; Ykase receptor.  
 DR Pfam; PF01404; Ephrin\_lbd; 1.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00536; SAM\_1; 1.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS00853; FN3\_2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; UNKNOWN\_1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS00105; SAM\_DOMAIN; 1.  
 KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;  
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.  
 FT NON TER 1  
 SQ SEQUENCE 815 AA; 90848 MW; D36D77C498097BFE CRC64;

Query Match 72.38; Score 3753.5; DB 2; Length 815;  
 Best Local Similarity 87.18; Pred. No. 4.4e-226;  
 Matches 710; Conservative 49; Mismatches 55; Indels 1; Gaps 1;

Qy 173 GFYLAFQDYGCCSLIAVRVYRKPRIIQNGAIFQETLSGAESTSLVAARGSCIANAE 232  
 Db 1 GFYLAFQDYGCCSLIAVRVYRKPRIIQNGAIFQETLSGAESTSLVAARGSCMPNAEE 60

Qy 233 VDVPILKYNCGDGLWLPVIGRCMKAGFAVENGTVCRCGSPGPFKANQGDCACTHCPIN 292  
 Db 61 VDVPILKYNCGDGLWLPVIGRCMKAGYSEVNGTVCRCGSPGPFKANQGDSDSLHCPIN 120

Qy 293 SRTTSGATNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGG 352  
 Db 121 SRTTSGATNCVCRNGYRADLPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGG 180

Qy 353 REDLVYNIICKSCGSGRGACTRCGDNVQVAPROLGLTEPRIYISDLAHTQYTFEIOAVN 412  
 Db 181 REDLVYHIICKSCGSGRGAYTHCGDNVQVAPROLGLTEPRIYISDLAHTQYTFEIOAVN 240

Qy 413 GVTDSQSPFQFASVNTTNOAPSAYSIMHQVSRVTSDITLSQDPQNGVILDYELQ 472  
 Db 241 GVTDSQSPFHSVNTTNOAPSAYSIMHLVTRADITSLSQDPQNGVILDYELL 300

Qy 473 YYEKELSEYNATAIKSTNTVTVOGLKAGAIYVQVARTVAGYGRYSGMYQFTWTEAE 532  
 Db 301 YDEKDLTEHNSRQSQSTNTVFLVGLRAGTIYVQVLSRRMAGYGRYSGMYQFTWTEAE 360

Qy 533 YQTSIQEKLFLIIGSSAAGLVFLIAVVIIVCN-RRGFRADSEYTDKLOHTSGHMT 591  
 Db 361 YQSSFOEKLFLIIGSSAAGLVFLIAVVIIVCSRGRFRADYEYTDKLOHTSGHMT 420

Qy 592 GMKIYIDPFYEDPNEAVREFAKEIDISCVKIEQVIGAGBEGEVCSEHKLKLPGRREIFVA 651  
 Db 421 GMKIYIDPFYEDPNEAVREFAKEIDISCVKIEQVIGAGBEGEVCSEHKLKLPXXREIFVA 480

Qy 652 IKTLKSGYTEKQRDFLSEASIMQFDPNVIHLEGVVTKSTPVIITEFMENGLSDSFL 711  
 Db 481 IKTLKSGYTEKQRDFLSEASIMQFDPNVIHLEGVVTKSTPVIITEFMENGLSDSFL 540

Qy 712 RQNDGQFTVIQLVGLMRLGIAAGMKYLADMYVVRDLAARNILVNSNLVCKVDSFGLSRFL 771  
 Db 541 RQNDGQFTVIQLVGLMRLGIAAGMKYLANMYVVRDLAAXNVLVNSNLVCKVDSFGLSRFL 600

Qy 772 EDDTSPTTYSALGGKIPRTWTAPEALQYRKFYSASVWSYGVIMVWVMSYGERPYWMT 831  
 Db 601 EDDTSPTTYSALGGKIPRTWTAPEALQYRKFYSASVWSYGVIMVWVMSYGERPYWMT 660

Qy 832 NQDVINAIEQDYRLPPPMDCPSALHOLMDCWQKDRNHRPKFGQIVNTLDKMIKRNPSLK 891  
 Db 661 NQSAIHAIVQDYRLPPPMDCPNALHQLLDQWQKDRNHRPKFGQIVNTLDKMIKRNPTIK 720

Qy 892 AMAPLSSGINLPLDRTIPDTYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMME 951  
 Db 721 AVAPLSSGVTPLDRTIPDTYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMME 780

Qy 952 DIILRGVTLACHOKKILNSIQVNRQMNQIQSVEV 986  
 Db 781 DIILRGVTLACHOKKILNSIQVNRQMNQIQSVEV 815

RESULT 15  
 EPBL\_CHICK  
 ID EPBL\_CHICK STANDARD; PRT; 984 AA.  
 AC Q07494;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ephrin type-B receptor 1 (EC 2.7.1.112) (Tyrosine-protein kinase  
 receptor EPH-2) (Tyrosine kinase CEK6 receptor) (fragment).  
 GN Names=EPH1; Synonyms=CEK6;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=93288394; PubMed=8510926;  
 RA Sajjadi F.G., Fasquale E.B.;  
 RT "Five novel avian Eph-related tyrosine kinases are differentially  
 expressed.";  
 RL Oncogene 8:1807-1813(1993).  
 CC -I- FUNCTION: Receptor for members of the ephrin-B family. Binds to  
 ephrin-B1, -B2 and -B3. May be involved in cell-cell interactions  
 in the nervous system.  
 CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 tyrosine phosphate.  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -I- TISSUE SPECIFICITY: Expressed at high levels in the 10-day embryo,  
 and in adult brain, lung, heart and skeletal muscle. Low levels of  
 expression detected in all other adult tissues tested.  
 CC -I- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
 receptor subfamily.  
 CC -I- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -I- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR ENBL; Z19110; CAA79526.1; -;  
 DR HSP; P54763; LUPA.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR003962; Ephrin\_subd.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR008979; Gal bind like.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008266; Tyr\_kinase AS.  
 DR InterPro; IPR001426; V\_kase\_receptor.  
 DR Pfam; PF01404; Ephrin\_lbd; 1.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; Kinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00615; EPH\_lbd; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; TyKc; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS50853; FN3; 2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; PARTIAL.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS50105; SAM\_DOMAIN; 1.  
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;  
 KW Transferase; Transmembrane; Tyrosine-protein kinase.  
 FT NON\_TER 1  
 FT DOMAIN <1 541 Extracellular (Potential).  
 FT TRANSMEM 542 562 Potential.  
 FT DOMAIN 563 984 Cytoplasmic (Potential).  
 FT DOMAIN 164 300 Cys-rich.  
 FT DOMAIN 304 405 Fibronectin type-III 1.  
 FT DOMAIN 411 525 Fibronectin type-III 2.  
 FT DOMAIN 619 882 Protein kinase.  
 FT DOMAIN 911 975 SAM.  
 FT SITE 982 984 PDZ-binding motif (Potential).  
 FT NP\_BIND 625 633 ATP (By similarity).  
 FT ACT\_SITE 651 651 ATP (By similarity).  
 FT BINDING 744 744 By similarity.  
 FT MOD\_RES 594 594 Phosphotyrosine (by autocatalysis) (Potential).  
 FT MOD\_RES 600 600 Phosphotyrosine (by autocatalysis) (Potential).  
 FT MOD\_RES 778 778 Phosphotyrosine (by autocatalysis) (Potential).  
 FT MOD\_RES 928 928 Phosphotyrosine (by autocatalysis) (Potential).  
 SQ SEQUENCE 984 AA; 109519 MW; EF06C83BB63A13A1 CRC64;

Query Match 71.7%; Score 3721; DB 1; Length 984;  
 Best Local Similarity 70.3%; Pred. No. 6.2e-224;  
 Matches 688; Conservative 121; Mismatches 150; Indels 20; Gaps 2;  
 21 ETLMDSITATAEALGVMHPPSGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKEIRR 80  
 1 ETLMDSITATAEALGWTANPPSGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKEIRR 60  
 81 RGAHRIHVMKFSVRDCSSIPSPGCKETFNLYYETDVIATKKSATFWTEAPYLKVDVT 140

Db 61 RGAHRIYTEMRTFVRDCSSIPSPGCKETFNLYYETDVIATKKSATFWTEAPYLKVDVT 120  
 Qy 141 IAADESFSQVDLGGRWKINTEVRSFGPVSRSFYLAQDYGGCMGLIIVRYFRCPRI 200  
 Db 121 IAADESFSQVDFGRLMKGXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXFFKPCPSV 180  
 Qy 201 IONGAIFQETLGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPVIGRCMKAGF 260  
 Db 181 VQNFALPPTMTGAESTSLVARGTCIPNAEVDVPIKLYCNGDGEWLVPVIGRCMKAGY 240  
 Qy 261 EAVENGTVCRGCPSTGTFKANOQDEACTHCPIINSRTTSEGATNCVCNRYRDLPLDMP 320  
 Db 241 EP-ENNVACRACFAGTFKASQAGLCAACPPNSRSSAEASPLCACRNGYFRADLDPTAA 299  
 Qy 321 CTIIPSAQAVISSVNSETSLMEWTTPRDSGGREDLVNII CKSCGSGACATCCGDNQ 380  
 Db 300 CTSVPSGPRNVISIVNETSIILEWNPRTGGDDVTYIVNCKKCRADRRACRCDNVE 359  
 Qy 381 YAPRQLGLTEPRIYISDILLAHTOYTFEIOAVNGVTDQSPFSPQFASVNTTNOAAPSAYS 440  
 Db 360 FVPRQLGLTETRVFISLWHTPYTFEIOAVNGVSNKSPFPPOHVSVNITTNOAAPSATVP 419  
 Qy 441 IMHVSRTVDSITLSWSQDPQNGVILDYELQYK-----ELSEY 481  
 Db 420 IMHVSATWRSITLSWPQEPQNGIILDYELRYEKLRICTPDVSGTVGSRPAADHNEY 479  
 Qy 482 NATAIKSPNTVTVOGLKAGAIYVOVARTVAGYSGKMYFOTWAEAYOTSIOEKL 541  
 Db 480 NSSVARSOQTARLEGLRFGVYVQVARTVAGYKISGKMCQFLLTDDDDYKSEUREQL 539  
 Qy 542 PLIGSSAAGLVPLIAVWIAIVCNRRGPERADSEYTDKLQHYTSGHMTGPKMIYIDPFT 601  
 Db 540 PLIAGSAAAGVPIVSLVAISIVCSRKRAYSEVVYSDKLQHYSTGRGSPGKMIYIDPFT 599  
 Qy 602 YEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTE 661  
 Db 600 YEDPNEAVREFAKEIDVSVFKIEBIVGAGEFGEVYKGRLLKLPKREIYVAIKTLKAGYSE 659  
 Qy 662 KQRDFLSEASIMGQFDHNVHLEGVVTKSTPVMIIITFMENGSLDSFLRQNDGQFTVI 721  
 Db 660 KQRDFLSEASIMGQFDHNIIRLEGVTVKSRPMIITFMENGALDLSFLRQNDGQFTVI 719  
 Qy 722 QLVGLRGIAGAGKYLADNMVYHRDLAARNILVSNLVCKVSDFLGSLFLEDDTSDPTYT 781  
 Db 720 QLVGLRGIAGAGKYLAEVYVHRDLAARNILVSNLVCKVSDFLGSLVQLDDTSDPTYT 779  
 Qy 782 SALGGKIPRTWTAPEAIQVRKFTSASDVWSYGIWMVEVMSYGERPYWDMNQDVINAIEQ 841  
 Db 780 SSLGGKIPVRWTAPEAIAYRKFTSASDVMSYGIWMVEVMSYGERPYWDMNSQDVINAIEQ 839  
 Qy 842 DYRLPPMDCPSALHOLMLDCWQDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGIN 901  
 Db 840 DYRLPPMDCPAALHQLMLDCWQDRNTPRLAEIVNTLDKMRNPASLTATVATVAPS 899  
 Qy 902 LPLDRTIPDYSFNTVDENLEAIKMGYKESFANAGFTSFDVVSQMMEDILRLGVTLA 961  
 Db 900 QPLDRSIPDFTAFSTVEDWLSAVKMSQYRDNFLSAGFTSLQLVAQWTSDDLRLIGVTLA 959  
 Qy 962 GHOKKILNSIQVNRQAMNQ 980  
 Db 960 GHOKKILNSIQSMRVQMSQ 978  
 RESULT 16  
 Q8CBE2 PRELIMINARY; PRT; 943 AA.  
 ID Q8CBE2 AC Q8CBE2;  
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length  
 DE enriched library, clone:9630045017 product:Eph receptor B1, full

DE insert sequence.  
GN Name=Ephbi;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayaishizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Mech. Enzymol. 303:19-44(1999).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN PANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RA The PANTOM Consortium;  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=2049374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayaishizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaishizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayaishida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayaishizaki Y.;  
RL Submitted (JUL-2001) to the ENBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
tyrosine phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
receptor subfamily.  
DE EMBL; AK036211; BAC29348.1; -.  
DR HSP; P54763; IJPA.

DR MGD; MGI:1096337; Ephbl.  
DR GO; GO:0005737; Cytoplasm; IDA.  
DR GO; GO:0016020; C-membrane; IDA.  
DR GO; GO:0008046; F-axon guidance receptor activity; IDA.  
DR GO; GO:0007411; P-axon guidance; IDA.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001090; Ephrin\_receptor.  
DR InterPro; IPR003962; FnlIII\_subd.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR InterPro; IPR011003; Kinase\_like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001660; SAM.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_kinase\_AS.  
DR InterPro; IPR001426; YKase\_receptorV.  
DR Pfam; PF01404; Ephrin\_lbd; 1.  
DR Pfam; PF00041; fn3; 2.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00536; SAM\_1; 1.  
DR PRINTS; PR00014; FNTYPEIII.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD001495; Ephrin\_receptor; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00615; EPH\_lbd; 1.  
DR SMART; SM00060; FN3; 2.  
DR SMART; SM00454; SAM; 1.  
DR SMART; SM00219; TykC; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
DR PROSITE; PS00853; FN3; 2.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR PROSITE; PS01005; SAM\_DOMAIN; 1.  
KW Glycoprotein; Kinase; Phosphorylation; Receptor; Transferase;  
KW Transmembrane; Tyrosine-protein kinase.  
SQ SEQUENCE 943 AA; 105324 MW; 5BC75B49D11139C2 CRC64;

Query Match 71.4%; Score 3705; DB 2; Length 943;  
Best Local Similarity 70.0%; Pred. No. 5.9e-233;  
Matches 682; Conservative 125; Mismatches 125; Indels 42; Gaps 2;  
QY 11 LLLPLAAVBETLMDSTTAAELGLWMVHPSPGVEEYSGYDENMNTITTYQVNVFESSQN 70  
DB 10 LLASAVANMEETLMDRTATAELOWTANPASGHEEYSGYDENLNTITTYQVNVFENQN 69  
QY 71 NWLRTKPIRRGAHRIHVMKFSVRDCSSIPSPGCKETFNLYYYEADFDATKTPNW 130  
DB 70 NWLLTPIRRGAHRIYTEMFTVRDCSSLPNVPGCKETFNLYYYETSDSVIATKKSFW 129  
QY 131 MENPWKVDITAADESFSQVDLGGVNMKINTEVRSFGVSRSGFYLAFOYGGCMSLIAY 190  
DB 130 SEAPYLKVDITAADESFSQVDFGRLMKVNTVRSFGPLTRNGFYLAFOYDYGACMSLLSV 189  
QY 191 RVFVRKCPRIIQNGAIFOETLSGAESTSLVAAGSCICIANAEVDVPIKLYCNGDGEWLVP 250  
DB 190 RVFVKKCPISQVNFVFPETMTGAESTSLVIAGTCIPNAEVDVPIKLYCNGDGEWNP 249  
QY 251 IGRCMCKAGFAEVNGTVCRCPSGTFCANQGDCAETHCPINRTTSEGATNCVCRNGYY 310  
DB 250 IGRCTCKPGYEP-ENSVACKACPAGTFKASQEAEGCSHCPSNSRSPSEASPICTCTGY 308  
QY 311 RADLDPLDMCTTIPSAPOAVISVNETSMLWETPRDSGGREDLVNLIICKSCSGRG 370  
DB 309 RADDFDPEVACTVPSGPRNVIISVNETSIILEWHHPRETGGRRDDVTYNTICKKCRADR 368  
QY 371 ACTRCGNVOYAPRQLGLTEPRIVISDLAHTTYVEIQAVNGVTQDPSFPOFASVNIT 430  
DB 369 SCGRCDNVFVPRQLGLTECRVISISLWHTPTTFDIOAINGVSSKSPFPQHVSNIT 428  
QY 431 TNOAFSAVSIHQVSRVTDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSPT 490



429	TNOAAPTVMQVSAITMSITLWQPEQNGIILDIYRIYKEHNEFSSMARSQT	488	RA	Jones S.J., Marra M.A.;
491	NTVTVOGLKAGAIYVFOVARTVAGYGRYGRMYFQMTAEAYOTSIQEKPLIIGSSAA	550	RT	"Generation and initial analysis of more than 15,000 full-length human
489	NTARIDGLRPGWVYVQVARTVAGYKFSKMKCFOTLTDYKSELREQLPLIAGSAAA	548	RL	and mouse cDNA sequences.";
551	GLVPLIAVIAVNCNRGRFERADSEYTDKLOHTSGHMTPGMKIYIDPTYEDPNEAVR	610	RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
549	GVFWFWSLVAISVCSRKRAYSKAAYSDKLOHYSTGR	586	RP	[2]
611	EPAKEIDISCVKIEQVIGAGEFGVCSGHLKLPKREIFVAIKTLKSGYTEKORRDFLSE	670	RC	SEQUENCE FROM N.A.
587	-----GEGEVYGRKLQKREIYVAIKTLKAGYSEKORRDFLSE	627	RA	Strausberg R.;
671	ASINGQDFHNPVHLEGVTKSTPVMIIITFPMENGSLDSFLRQNDGQFTVIQLVGMLRGI	730	RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
628	ASINGQDFHNPVHLEGVTKSTPVMIIITFPMENGALDSFLRQNDGQFTVIQLVGMLRGI	687	CC	-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
731	AAGKYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTVTSALGGKIPV	790	CC	tyrosine phosphate.
688	AAGKYLSEMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTVTSALGGKIPV	747	CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
791	RWTAPEAIQYKFTSASDVMSYGIWVMEVMSYGRPYWDMNQVINAIQDYRLPPPPMD	850	CC	-I- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
748	RWTAPEAIYKFTSASDVMSYGIWVMEVMSYGRPYWDMNQVINAIQDYRLPPPPMD	807	CC	receptor subfamily.
851	CPSALHQLMDCWKDRNRHPKFCQIVNTLDKMRNPNLSKAMAPLSSGGINLPLDRTIP	910	DR	EMBL: BC052968; AAHS2968.1; --
808	CPSALHQLMDCWKDRNRHPKFCQIVNTLDKMRNPNLSKAMAPLSSGGINLPLDRTIP	867	DR	GO: GO:0016021; C: integral to membrane; IEA.
911	DYTSFNTVDEWLEAIKMGQYKESFANAGTSFSDVVSQMMEDILRLGVLGAGHOKILNS	970	DR	GO: GO:0005524; F: ATP binding; IEA.
868	DFTAFVTDDWLSAKWQYKDSFLTAGFTSLQVLTQNTSEDLRLGVLGAGHOKILNS	927	DR	GO: GO:0005003; F: Ephrin receptor activity; IEA.
971	IQVNRQANQIQSV 984		DR	GO: GO:0004713; F: protein-tyrosine kinase activity; IEA.
928	IHSRMVQNQSPSV 941		DR	GO: GO:0004872; F: receptor activity; IEA.
RESULT 17				
Q72740				
ID	Q72740	PRELIMINARY;	PRT;	998 AA.
AC	Q72740;			
DT	01-OCT-2003 (TrEMBLrel. 25, Created)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Ephrin receptor EphB3.			
GN	Name=EphB3;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Uterus;			
RC	MEDLINE=22388257; PubMed=12477932;			
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettunen M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,			



Qy	244	DG	ENLPIGR	CHCKAGFAVENGV	VCRCPSGT	PFKANGDBEACH	CPINSRTT	SEGA	TNC	303			
Db	259	DG	EMVVPV	GACTCATG	HEPAKESQCR	PPGSGKQGE	GCPLPCP	PNSTRTT	SPAAS	318			
Qy	304	VC	RNGYR	ADLDPLD	MPCTTIP	SAPOAVISSVNET	SLMLEWT	PPDSGG	DLAVN	363			
Db	319	TH	NNFYR	ADSDASACT	TTPSP	PPRGV	ISNVNET	SIL	EWSEPR	DUGG	DDLUNV	378	
Qy	364	SC	-GSGR	GACTRC	GDNVQYAP	RLGLTEPR	PIYISD	LLAHTQ	TYTTEI	QA	VNGVTD	SPFS	421
Db	379	KCH	GAGGAS	ACSRCDN	VEFPV	RLGLTERR	VHISHL	LAHTRY	TTFE	VQA	VNGVSG	KSLP	438
Qy	422	PO	PASV	NTTNOA	QASVIM	QHVSR	TVDSIT	LSNSOP	DPDQ	PNGV	LDYELQ	YETK	481
Db	439	PR	YAAV	NTTNOA	PSEVPT	LRLLSS	SGSSIT	LSWAPP	PNGV	LDYELQ	YETK	481	496
Qy	482	NATA	KSPNT	VTVGL	KAGAIY	FOVPA	RVAG	RYG	SKWY	FO	TWTE	-AEYQ	540
Db	497	IAS	TVTSQ	MNSVQL	DGLRDP	ARYVQV	RVART	VAGYQ	TSP	PAEFT	T	SE	556
Qy	541	LPL	IGSSA	AGI	VLFI	AVVIA	VIAV	CNRR	GER	PER	ADSEY	T	600
Db	557	LPL	IGS	ATAG	LFFV	AVVIA	VIAV	CLRK	QRHGS	DSEY	T	KLQY	612
Qy	601	TYED	NEA	VREPA	KIDIS	CVK	IEBO	VIGAG	BEF	GVCS	GHKL	PK	660
Db	613	TYED	NEA	VREPA	KIDIS	CVK	IEBO	VIGAG	BEF	GVCS	GHKL	PK	672
Qy	661	EXOR	DF	FE	ASIM	QFO	PHNV	IHL	EGV	VTK	TPM	IL	720
Db	673	EXOR	DF	FE	ASIM	QFO	PHNV	IHL	EGV	VTK	TPM	IL	732
Qy	721	IQLV	GLM	RGIA	AGMKY	LADMN	VVHR	DLA	ARNIL	VNS	NLVCK	VSD	780
Db	733	IQLV	GLM	RGIA	AGMKY	LSEMY	VHRD	LA	ARNIL	VNS	NLVCK	VSD	792
Qy	781	TSAL	GK	PIR	TAPEA	IQYR	KFTS	ASDV	WSY	GIV	MMVMSY	G	840
Db	793	TSAL	GK	PIR	TAPEA	IQYR	KFTS	ASDV	WSY	GIV	MMVMSY	G	852
Qy	841	QYR	LP	PP	PN	MD	CP	SALH	OLM	CD	CK	DR	900
Db	853	QYR	LP	PP	PN	MD	CP	SALH	OLM	CD	CK	DR	912
Qy	901	NLP	LD	RT	PD	YTS	FN	TVD	LEA	LK	MG	QY	960
Db	913	SQ	PL	DR	TP	VD	YTS	FN	TVD	LEA	LK	MG	972
Qy	961	AGH	QK	IL	NSI	QV	MA	RNNQ	ISQ	VEV	986		
Db	973	AGH	QK	IL	NSI	QV	MA	RNNQ	ISQ	VEV	986		
RESULT 18													
EPB3 CHICK													
ID	EPB3	CHICK	STANDARD;				PRT; 988 AA.						
AC	Q074	98;											
DT	16-OCT-2001	(Rel. 40, Created)											
DT	16-OCT-2001	(Rel. 40, Last sequence update)											
DE	05-JUL-2004	(Rel. 44, Last annotation update)											
DE	Ephrin type-B receptor 3 (BC 2.7.1.112) (Tyrosine-protein kinase receptor CEK10) (Fragment)												
DN	Name=EPHB3; Synonyms=CEK10; Gallus gallus (Chicken)												
OS	Gallus gallus (Chicken)												
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus												
OC	Gallus												
NCBI	TaxID=9031;												
RN	SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).												
RP	TISSUE=Embryo;												
RC	MEDLINE=93288394; PubMed=8510926;												
RX	Sajjadi F.G., Pasquale E.B.;												
RA													

"Five novel avian Eph-related tyrosine kinases are differentially expressed.";  
 Oncogene 8:1807-1813(1993).  
 -!- FUNCTION: Receptor for members of the ephrin-B family.  
 -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.  
 -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 -!- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named isoforms=2;  
 Name=Long;  
 IsoId=Q07498-1; Sequence=Displayed;  
 Name=Short;  
 IsoId=Q07498-2; Sequence=VSP\_003019;  
 Note=No experimental confirmation available;  
 -!- TISSUE SPECIFICITY: Present in 10-day embryonic brain and body tissues. Prominent expression in kidney. Lower expression in lung, and barely detectable in brain, liver, heart, skeletal muscle and thymus.  
 -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.  
 -!- SIMILARITY: Contains 2 fibronectin type III domains.  
 -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 -----  
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 EMBL; Z19061; CAA79511.1; -;  
 PIR; I50611; I50611.  
 HSPG; P54763; 1JUPA.  
 InterPro; IPR001090; Ephrin\_receptor.  
 InterPro; IPR003962; FNIII\_subd.  
 InterPro; IPR003961; FN\_III.  
 InterPro; IPR008957; FN\_III-like.  
 InterPro; IPR008979; Gal\_bind\_like.  
 InterPro; IPR011009; Kinase\_like.  
 InterPro; IPR000719; Prot\_kinase.  
 InterPro; IPR001660; SAM.  
 InterPro; IPR001245; Tyr\_kinase.  
 InterPro; IPR008266; Tyr\_kinase\_AS.  
 InterPro; IPR001426; YKase\_receptorV.  
 Pfam; PF01404; Ephrin\_lbd; 1.  
 Pfam; PF00041; fn3\_2.  
 Pfam; PF00063; Pkinase; 1.  
 Pfam; PF00536; SAM; 1.  
 PRINTS; PR00014; FNTYPEIII.  
 PRINTS; PR00109; TYRKINASE.  
 ProDom; PD001495; Ephrin\_receptor; 1.  
 ProDom; PD000001; Prot\_kinase; 1.  
 SMART; SM00615; EPH\_lbd; 1.  
 SMART; SM00060; FN3; 2.  
 SMART; SM00454; SAM; 1.  
 SMART; SM00219; TyrKc; 1.  
 PROSITE; PS50853; FN3; 2.  
 PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 PROSITE; PS50105; SAM\_DOMAIN; 1.  
 Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;  
 Receptor; Repeat; Transferrase; Transmembrane; Tyrosine-protein kinase.  
 -----  

NON_TER	1	1
DOMAIN	<1	534
TRANSMEM	535	555
DOMAIN	556	988
DOMAIN	171	308
DOMAIN	312	416
DOMAIN	426	518

  

Extracellular (Potential).	
Potential.	
Cytoplasmic (Potential).	
Cys-rich.	
Fibronectin type-III 1.	
Fibronectin type-III 2.	



```

DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001560; SAM_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase AS.
DR InterPro; IPR001426; Ykase receptorV.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3_2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 33
FT CHAIN 34 998
FT DOMAIN 34 559
FT TRANSMEM 560 580
FT DOMAIN 581 998
FT DOMAIN 199 336
FT DOMAIN 340 443
FT DOMAIN 453 544
FT DOMAIN 633 896
FT DOMAIN 925 989
FT SITE 996 998
FT NP_BIND 639 647
FT BINDING 665 665
FT ACT_SITE 758 758
FT MOD_RES 608 608
FT MOD_RES 614 614
FT MOD_RES 792 792
FT MOD_RES 942 942
FT CARBOHYD 351 351
FT CARBOHYD 445 445
FT SEQUENCE 998 AA; 110286 MW; 57C92C397CC61103 CRC64;

Query Match
Best Local Similarity 70.2%; Score 3661.5; DB 1; Length 998;
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;

Qy 10 LLLPL-----AAVEETLMDSTATAELGMMVHPSPGMEVSGYDENMNTIRYQVCN 63
Db 23 LLLPLLLPAGCRALBETLMDTKWVTSALWTSHPESGMEVSGYDEAMNPIRTYQVCN 82
Qy 64 VFSSQNNLTKFIRRGARHIVEMKFSVRDCSSIPSPGCKETFNLYFYEADPDSA 123
Db 83 VRESSQNNLTKFIRWRDQVVRVVELKFTVRDCNSIPNIPGCKETFNLYFYEADSDVA 142
Qy 124 TKTPNNMENPWKVDITAADESFQVDLGRVKNKINTEVRSGFVSRSGFYLAFOYGG 183
Db 143 SASPFWMENPYKVDITAPDESRLDAG-----RVNTKVRSGFPLSKAGFYLAFOQGA 198
Qy 184 CMSLIARVFRYKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 243

199 CMSLISVRAFYKKCASTTAGFALPETLTGAETPTSLVIAPTCIPNAVEVPLKLYCNG 258
244 DGEWLVPGRGCKAGFEAVENGIVCRGCPSTGTPKANQGDDEACTHCPINSETTSEGATNC 303
259 DGEWVVPVGAAGTCAATGHEPAKESQCRPCPPGSKYAKQGGFCPLPCPNSTTTSPAASIC 318
304 VCRNGYTRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGREDLVNITCK 363
319 TCHNFRADSDSADSACTIVPSPRGVSNVNETSLILEWSEPRDLGVRDLDLNVICK 378
364 SC--GSGRGACTRCGDNVQYAPROLGLTEPRIYISDLAHTQYTFEQAQVNGVTDQSPFS 421
379 KCHGAGGASACRCDNDVFEVPRGLSEPRVHTSHLLAHTRYTFEVAQVNGVSGKSLP 438
422 POPASVNITNOAAPSASVIMHQVSRVDSITLWSOPDOPNGVILDYELQYKEKSEY 481
439 PRYAANVITNOAAPSEVPTLRHSSGSSLTLSWAPPRNGVILDYEMKYPK--SEG 496
482 NATAIKSPNTNTVTVOGLKAGAIYVQVARTVAGYGRYSGMYPQTMTAEYQTSIQEK 540
497 IASTVTSQMSVQLDGLRDPARYVQVARTVAGYGRYSPAEFETTSERSGGAQQLQEQ 556
541 LPLIIGSSAAGLPLIAVVIIVCNRRGPERADSEYTDKLOHTSGHMTPGMKIYIDPF 600
557 LPLIVGSATAGLVFVAVVIAIVCLRKQRHGSSEYTEKLQY----IAPGMKVIYIDPF 612
601 TYEDPNEAVREFAKEIDISCVKLEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKTKSGYT 660
613 TYEDPNEAVREFAKEIDVSCVKIEEVIAGEFGEVCRGLKQGRREVFVAIKTKVGYT 672
661 EKORRDFLSEASIMGQFDHNVNHLGVTKSTPVMITTEFMENGSLDSFLRQNDGQFTV 720
673 ERQRDFLSEASIMGQFDHNIIELEGVTKSRPVMITTEFMENCALDSFLRNDGQFTV 732
721 IQLVGLRGIAAGKYLADMYVHRDLAARNILVSNLVCVKVSDFGLSRLEDDTSDPTY 780
733 IQLVGLRGIAAGKYLSENNYVHRDLAARNILVSNLVCVKVSDFGLSRLEDDTSDPTY 792
781 TSALGGKIPRWTAPEAIQYRKETSASDVMSYGVIMVMSYGERPYWDMNQDVINAIE 840
793 TSLGGKIPRWTAPEAIYRKETSASDVMSYGVIMVMSYGERPYWDMNQDVINAIE 852
841 QDVLRLPPMPCPSALHOLMDCQKDRNHRPKFGQIVNTLDKMRNPNLSKAMAPLSGI 900
853 QDYELPPMPCPTALHQLMDCWRDRNLRPKSQIVNTLDKLRNAASLVKIASAOSGM 912
901 NLPLLDRTIPDYSFNTVDWLEBAIKMGQYKESFANAGFTSFVVSQMMMEDILRLGVTL 960
913 SQPLLDRTVPDYTTFTTVGDWLDIAKMGYKESFVSAGFASFDLVAQMTAEDLLRIGVTL 972
961 AGHQKILNSIOVWRAQMNQIQSVEV 986
973 AGHQKILSLSIQDRLQMNQTLPPQV 998

RESULT 20
Q91YS9
ID Q91YS9 PRELIMINARY; PRT; 993 AA.
AC Q91YS9;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Eph receptor B3.
GN Name=Ephb3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N, and C57BL/6; TISSUE=Brain, and Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932;

```

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
 CC receptor subfamily.  
 DR EMBL; BC014822; AAH14822.1; -;  
 DR EMBL; BC053085; AAH53085.1; -;  
 DR HSP; P54763; 1JPA.  
 DR MGD; MGI:104770; Ephb3.  
 DR GO; GO:0008046; P:axon guidance receptor activity; IDA.  
 DR GO; GO:0007411; P:axon guidance; IDA.  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR003962; FcIII subd.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR008979; Gal bind like.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008266; Tyr\_kinase AS.  
 DR InterPro; IPR001426; Vase\_receptor.  
 DR Pfam; PF01404; Ephrin\_lbd; 1.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00536; SAM 1; 1.  
 DR PRINTS; PR00014; FNTYPIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00615; EPH\_lbd; 1.  
 DR SMART; SM00454; SAM; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00853; FN3; 2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS0105; SAM\_DOMAIN; 1.  
 KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;  
 KW Transferase; Transmembrane; Tyrosine-protein kinase.

SQ SEQUENCE 993 AA; 109661 MW; 07C6EF2AC98AE1B4 CRC64;  
 Query Match 70.5%; Score 3657.5; DB 2; Length 993;  
 Best Local Similarity 70.0%; Pred. No. 5.9e-220;  
 Matches 692; Conservative 114; Mismatches 162; Indels 21; Gaps 6;  
 9 ALLLPLLA-----AVEETLMDSTTATAELGWMVHPPSPGSGWEEVSGYDENNTIRTYQVCN 63  
 15 APLLPLLLPAGCWALEETLMDTKWVTSBLAWTSHPESGWEEVSGYDEAMNPIRTYQVCN 74  
 64 VFESSQNNWLRTKFIPTRRGAHRIHVMKESVDCSSIPVPGSCKETENLYYEADFDSA 123  
 75 VRESSQNNWLRTGFIWRREVQRYVELKFTVDCNSIPNPGSCKETENLYYEADFDSA 134  
 124 TKTFPNNMENPWKVDVTIAADESFQVDLGGRWKINTVRSFGPVSRSGFYLAFOYGG 183  
 135 SASSPFWMENPVKVDVTIAPDESFSRLDAG----RVNTKVSFGPLSKAGFYLAFOQGA 190  
 184 CMSLIAVRVYFKCPRIIQNGAIFQETLSGASTSLVAARGSCIANAEVDPVKLYCNG 243  
 191 CMSLISVRAFYKKCASTTAGFALFPETLTGAPTSLVIAPTGCIANAEVSVPLKLYCNG 250  
 244 DGEWLVPICRCWKAGFAVENGTVCRCGPGSGTFFKANQGDCACTHCPINSRTTSECATNC 303  
 251 DGEWMPVVGACTCATGHEPAKESQCRACPPGSKAKQGEPCPCPPNSRTTSPASIC 310  
 304 VCRNGYVRADLPDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICK 363  
 311 TCHNFYRADSDSADSACTVSPPRGVISNVNETSLILEWSEPRDLGGRDDLLYNVICK 370  
 364 SCGSGRGA-----CTRCGNQVAPQQLGLTPRIYISDLAHTQVTFIQAQNGVTDQS 418  
 371 KCRGSGAGGATPCSCDDNVFPRQLGLTERRVHSHLLAHTRYTFEVAQVNGVSGKS 430  
 419 PESPQASVNIITNQAPSAVSIMHOVSRTVDSITLSWSQDPQNPQNVILDYELQYKEKEL 478  
 431 PLPRYAANVTINQAPSEVPTLHLHSSGSLTUSWAPPERNGVILDYENKYEK-- 488  
 479 SEYNATAIKSPNTVTVOGLKAGAIYVQVARTVAGYGRYSGMKYFQMTWE--AEYQTSI 537  
 489 SKGIASVTTSQKNSVQLDGLQPDARVYVQVARTVAGYGOYSHPAEFETTSERGSQAQ 548  
 538 QEKPLIIGSSAAGLVFLIAVVIATVCMRPFERADSEYTDKLOHTYTSCHMTPGMKIYI 597  
 549 QEOLPLIVGSTVAGFVFMVVVIALVCLRKQKHGPDABYTEKLOQY----TAPGMKVYI 604  
 598 DPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKS 657  
 605 DPFTYEDPNEAVREFAKEIDVSCVKEEVIGAGEFGEVCGRLKLPGRREVFAIKTLKV 664  
 658 GYTEKQRDFLSEASIMGQFDHPNVIHLEGVWTKSTPVMITTEFMNGSLDSFLRNDGQ 717  
 665 GYTERQRDFLSEASIMGQFDHPNIIRLEGVWTKSRPVMILTEFMENCALDSFLRNDGQ 724  
 718 FTVIQVLMRLGIAAGKYLADNMYVHRLAARNILVNSNLCKVSDGFLSRLEDDTSD 777  
 725 FTVIQVLMRLGIAAGKYLSENNYVHRLAARNILVNSNLCKVSDGFLSRLEDDTSD 784  
 778 PTVTSALGGKIPIRTWTAPEAIOYRKFTSADVMSYGIVMWEVMSYGERPDMTNDQVIN 837  
 785 PTVTSALGGKIPIRTWTAPEAIAIRKFTSADVMSYGIVMWEVMSYGERPDMTNDQVIN 844  
 838 AIEQDYRLPPMDPCPSALHQLMDCQKORNRHPKFGQIVNTLDKMRNPNSLKAMAPLS 897  
 845 AVEODYRLPPMDPCPTALHQLMDCQKORNRHPKFSQIVNTLDKIRNAASLKVTASAP 904  
 898 SGINLPLIDRTIDYTSFNTVDEWLEAIKMGQVKESFANAGFTSDVVSMMEDILRLG 957  
 905 SGMSQPLLDRTVPDYTFITVGVNLDKMRNPNSLKAMAPLS 964  
 958 VTLAGHOKKILNSIQVNRQAQNIQSV 986  
 965 VTLAGHOKKILCSIQDMRLQMNQTLFPQV 993

## RESULT 21

ID\_EBP3\_MOUSE STANDARD; PRT; 993 AA.  
 AC P54754; Q62214;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ephrin type-B receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein  
 DE kinase receptor MDK-5) (Developmental kinase 5) (SEK-4).  
 GN Name=Ephb3; Synonyms=Eck2, Mdk5, Sek4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Embryo;  
 RX MEDLINE=96074837; PubMed=7478528;  
 RA Closssek T., Lerch M.M., Ullrich A.;  
 RT "Cloning, characterization, and differential expression of MDK2 and  
 RT MDK5, two novel receptor tyrosine kinases of the eck/eph family.";  
 RL Oncogene 11:2085-2095 (1993).  
 RN [2]  
 RP SEQUENCE OF 719-993 FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=95034306; PubMed=7947319;  
 RA Becker N., Seitanidou T., Murphy P., Mattei M.-G., Topilko P.,  
 RA Nieto A., Wilkinson D.G., Charnay P., Gilaradi P.;  
 RT "Several receptor tyrosine kinase genes of the Eph family are  
 RT segmentally expressed in the developing hindbrain.";  
 RL Mech. Dev. 47:3-17 (1994).  
 RN [3]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20171264; PubMed=10704386;  
 RA Imondi R., Wideman C., Kaprielian Z.;  
 RT "Complementary expression of transmembrane ephrins and their receptors  
 RT in the mouse spinal cord: a possible role in constraining the  
 RT orientation of longitudinally projecting axons.";  
 RL Development 127:1397-1410 (2000).  
 CC -1- FUNCTION: Receptor for members of the ephrin-B family.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in cells of the retinal ganglion  
 CC cell layer during retinal axon guidance to the optic disk.  
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
 CC receptor subfamily.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; Z49086; CAA89910.1; -;  
 DR EMBL; X76012; CAA53599.1; -;  
 DR PIR; I48653; I48653.  
 DR PIR; I48761; I48761.  
 DR HSP; P54763; LUPA.  
 DR MGD; MG1104770; Ephb3.  
 DR GO; GO:0008046; F:axon guidance receptor activity; IDA.  
 DR GO; GO:0007411; P:axon guidance; IDA.  
 DR InterPro; IPR001090; Ephrin receptor.  
 DR InterPro; IPR003962; FNIII subd.  
 DR InterPro; IPR003961; FN III.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR008979; Gal\_bind\_like.

DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008266; Tyr\_kinase\_AS.  
 DR InterPro; IPR001426; Ykase\_receptorV.  
 DR Pfam; PF01404; Ephrin\_lbd; 1.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00615; EPH\_lbd; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS00853; FN3; 2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS0105; SAM\_DOMAIN; 1.  
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;  
 KW Transferase; Transmembrane; Tyrosine-protein kinase.  
 FT SIGNAL 1 29 Potential.  
 FT CHAIN 30 993 Ephrin type-B receptor 3.  
 FT DOMAIN 30 554 Extracellular (Potential).  
 FT TRANSMEM 555 575 Potential.  
 FT DOMAIN 576 993 Cytoplasmic.  
 FT DOMAIN 191 328 Cys-rich.  
 FT DOMAIN 332 438 Fibronectin type-III 1.  
 FT DOMAIN 448 539 Fibronectin type-III 2.  
 FT DOMAIN 628 891 Protein kinase.  
 FT DOMAIN 920 984 SAM.  
 FT SITE 991 993 PDZ-binding motif (Potential).  
 FT NP\_BIND 634 642 ATP (By similarity).  
 FT BINDING 660 660 ATP (By similarity).  
 FT ACT\_SITE 753 753 By similarity.  
 FT MOD\_RES 603 603 Phosphotyrosine (by autocatalysis) (By  
 FT similarity).  
 FT MOD\_RES 609 609 Phosphotyrosine (by autocatalysis) (By  
 FT similarity).  
 FT MOD\_RES 787 787 Phosphotyrosine (by autocatalysis)  
 FT (Potential).  
 FT MOD\_RES 937 937 Phosphotyrosine (by autocatalysis) (By  
 FT similarity).  
 FT CARBOHYD 343 343 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 440 440 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 719 719 R -> Q (in Ref. 2).  
 SQ SEQUENCE 993 AA; 109585 MW; 0B66A4D391266C79 CRC64;  
 Query Match 70.0%; Score 3630.5; DB 1; Length 993;  
 Best Local Similarity 69.8%; Pred. No. 2.9e-218;  
 Matches 690; Conservative 113; Mismatches 165; Indels 21; Gaps 6;  
 QY 9 ALLLLPILA-----AVETLMDSTTATAEIGWVHPSPSGWEEVSGYDENNTTITYQVCN 63  
 DB 15 APLLPPLLPAGCWALEETLMDTKWVTSWTSHPESGWEEVSGYDENNTTITYQVCN 74  
 QY 64 VPSSQNNWLRTEFIRRRGAHRTHVEMKFSVRDCSSIPSPVPGSKETFNLYYEADPDSA 123  
 DB 75 VRESSQNNWLRTEGFIWRREVQRYVVELKFTVRDCNIPINPGSKETFNLYYEASDVA 134  
 QY 124 TKTFPNNMENPWKVDITIAADESFSQVDLGGRRVKINTEVRSFGPVSRSFGYLAFOYGG 183  
 DB 135 SASSPFWMENPYVKVDITAPDESFSRLDAG----RVNTKRSFGPLSKAGFYLAFOQGA 190  
 QY 184 CMSLIAVRVYFKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVIFKLYCNG 243  
 DB 191 CMSLISVRAGDKKCASTTAGFALPETLTGAETPSLVIAPGTCTIANAEVSVPLKLYCNG 250

244 DGEWLVPGRMCAGPEAVENGTVCRGCPGTGFKANQGDCACTHCPINSRTTSEGATNC 303  
251 DGEWVVPVGAICTCATGHEPAKESQCRACPGSVKAKQGGPCLPCPPNSRTTSPASIC 310  
304 VCRNGYVRADLPDMPCTTTPSAPQAVISSVNNETSLMLEWTPPRDSGGREDIYVNIICK 363  
311 TCHNPFYRADSDSADSACTTEPSPRGVSNVNETSLILEWSEPRDLGGRDLLYNVICK 370  
364 SCGSGRA-----CTRCGDNVQAPROGLTETPRIVISDLIAHTOTTFELQAVNGVTDQS 418  
371 KCRGSSGAGGATPCSCRDDNVFVPRQLGTERVHSHLAHTRYTFEQAVNGVSGKS 430  
419 PFSPOFASVNTTNOAAPSASVIMHQSRTVDSITLWSQPDOPNGVILDYELQYVEKEL 478  
431 PLPRYRANVTITNOAAPSEVPLHLHSSGSLTILSWAPPRNGVILDYEMKYEK-- 488  
479 SEYNATAIKSFTNTVTVQGLKAGAIYVQVARTVAGYRGYSGMYQVPTWTE-AYQTSI 537  
489 SKGIASVTVSQKNSVQLDGLQPDARYVQVQVARTVAGYQYSHPAEPETTSSRGSGAQQL 548  
538 QEKPLIIGSAGLVFLIAVVTIAVCNRRGERADSEVTDKLOHYTSGHMTPGMKIYI 597  
549 QEQPLVIGSVTAVGFVFMVWVVALVCLQRQRGPDAYTEKLLQY-----IAPGMKVYI 604  
598 DPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSCHLKLPGKREIFVAIKTKS 657  
605 DPFTYEDPNEAVREFAKEIDVSCVKIEBEVIGAGEFGEVCGRLKLPGRREVFVAIKTKV 664  
658 GYTEKORRDLSEASIMGQFDHPNVHLEGVVTGKSTPVMITITFMENGSLDSFLRQNDGQ 717  
665 GYTERQRDRFLSEASIMGQFDHPNIIRLEGVVTGKSRPVMILITFMENCALDSFLRLNDGQ 724  
718 FTVIQLVGLRGIAAGMKYLADNMVYHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSD 777  
725 FTVIQLVGLRGIAAGMKYLSEMYVYHRDLAARNILVNSNLVCKVDFGLSRFLEDDPSD 784  
778 PTYSALGKPIPIRTWTAPEAIQVRKFTSASDVMSYGIWMVEVMSYGERPYWDMTNQDVIN 837  
785 PTYTSLSGKPIPIRTWTAPEAIYKFTSASDVMSYGIWMVEVMSYGERPYWDMNSQDVIN 844  
838 AIEQDYLPMPDPCPSALHQLMDCWQKDNHRPKFQIVNTLDKMTNRNPSLKAMAPLS 897  
845 AVEQDYLPMPDPCPTALHQLMDCWVRDRNLKPKFSQIVNTLDKLRNAASLKVTASAP 904  
898 SGINLPILDRTPIDYTSFNTVDEWLEAIKMGYKESFANAGFTSFVVSQMMEDILRLG 957  
905 SGMSQPLDRTPIDYTSFNTVDEWLEAIKMGYKESFVGGAFASFDLVQMTAEDLLRIG 964  
958 VTLAGHQRKILNSIQVNRQMNQIQSVEV 986  
965 VTLAGHQRKILNSIQVNRQMNQILPQV 993

RESULT 22  
EPBB XENLA  
ID EPBB XENLA STANDARD; PRT; 902 AA.  
AC Q91736;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ephrin type-B receptor 1B (EC 2.7.1.112) (Tyrosine-protein kinase receptor XELK) (Fragment).  
DE Name=XELK;  
GN Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96068901; PubMed=7478602;  
RA Scales J.B., Winning R.S., Renaud C.S., Shea L.J., Sargent T.D.;

RT Novel members of the eph receptor tyrosine kinase subfamily expressed during Xenopus development.";  
RL Oncogene 11:1745-1752(1995).  
CC 1- FUNCTION: Receptor for members of the ephrin-B family (By similarity).  
CC 1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.  
CC 1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC 1- TISSUE SPECIFICITY: Expressed in the embryo in the brain and spinal cord and in the first and fourth visceral arches. Most abundant in adult brain, with lower levels in eye, heart, ovary, oviduct, lung and pharynx.  
CC 1- DEVELOPMENTAL STAGE: Expressed during early development.  
CC 1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.  
CC 1- SIMILARITY: Contains 2 fibronectin type III domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; L43621; AAA33527.1; -;  
CC HSSP; P54763; 1JPA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001090; Ephrin receptor.  
DR InterPro; IPR003922; FNIII\_subd.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR008979; Gal bind like.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR00719; Prot\_kinase.  
DR InterPro; IPR01660; SAM.  
DR InterPro; IPR01245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_kinase\_AS.  
DR InterPro; IPR001426; YKase\_receptorV.  
DR Pfam; PF01404; Ephrin\_lbd\_1.  
DR Pfam; PF00041; fn3\_2.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00536; SAM; 1.  
DR PRINTS; PR00014; FNTYPEIII.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD001495; Ephrin\_receptor; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00615; EPH\_lbd; 1.  
DR SMART; SM00600; FN3\_2.  
DR SMART; SM00454; SAM; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS00853; FN3\_2.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR PROSITE; PS0105; SAM\_DOMAIN; 1.  
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;  
KW Transferase; Transmembrane; Tyrosine-protein kinase.  
FT NON\_TER 1  
FT DOMAIN <1 459 Extracellular (Potential).  
FT TRANSMEM 460 480 Potential.  
FT DOMAIN 481 902 Cytoplasmic (Potential).  
FT DOMAIN 101 237 Cys-rich.  
FT DOMAIN 241 342 Fibronectin type-III 1.  
FT DOMAIN 352 443 Fibronectin type-III 2.  
FT DOMAIN 537 800 Protein kinase.  
FT DOMAIN 829 893 SAM.  
FT SITE 900 902 PDZ-binding motif (Potential).  
FT NP\_BIND 543 551 ATP (By similarity).  
FT BINDING 569 569 ATP (By similarity).

FT	ACT_SITE	662	By similarity.
FT	MOD_RES	512	Phosphotyrosine (by autocatalysis)
FT		518	(Potential).
FT	MOD_RES	518	Phosphotyrosine (by autocatalysis)
FT		596	(Potential).
FT	MOD_RES	596	Phosphotyrosine (by autocatalysis)
FT		846	(Potential).
FT	MOD_RES	846	Phosphotyrosine (by autocatalysis)
FT		252	(Potential).
FT	CARBOHYD	344	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	398	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	398	N-linked (GlcNAc. . .) (Potential).
FT	SEQUENCE	902 AA; 100850 MW; CCBABF7D39273CA CRC64;	
Qy	Query Match	69.6%; Score 3612.5; DB 1; Length 302;	
Db	Best Local Similarity	73.2%; Pred. No. 3.4e-217;	
Db	Matches	658; Conservative 127; Mismatches 109; Indels 5; Gaps 3;	
Qy	84	HRHVENKFSVRDCSSIPSPVSGCKETFNLYYYEAD--FDSATYTFPWNWNPWKVDTTI 141	
Db	1	HRVYVENRFTVRDCSSLPSPVSGCKETFNLYYYETDSNIDNKISTF--WNESPYLKVDTTI 58	
Qy	142	AADSEFSQVDLGGKVMKINTEVRSGFVPSRSGFYLAQDYGGWLSLIAVRFVKKCPRII 201	
Db	59	AADSEFSQVDLGGKVMKINTEVRSGFVPSRSGFYLAQDYGGWLSLIAVRFVKKCPRII 118	
Qy	202	QNGAIFQETLSGAEBSLVAARGSCIANABEVDVPIKLYCNGDGEWLVPIGRCKCKAGFE 261	
Db	119	QNFVAVFETWTGAEBSLVAARGSCIANABEVDVPIKLYCNGDGEWLVPIGRCKCKAGFE 178	
Qy	262	AVENGTVCRGCPSTFKANGDDEACTHCPIINSRTSGATNCVCRNGYRRAADLDPLMPC 321	
Db	179	P-ENHVYVCKAPAMFRANQMGICCAQCPANSRSTSEASPTICIRNGYRRADEFTPEAPC 237	
Qy	322	TTTSPAQAVTSVSNVETSLMEWTPRDSGREDLVNIIICKSCSGRGACTRCGDNVQY 381	
Db	238	TSPVSGPRNVISIVNETAITLEWHPPRTGDRDNNIICKSCSGRGACTRCGDNVQY 297	
Qy	382	APROLGTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFQFASVNIITNQAAAPSIVI 441	
Db	298	VPRLGLTDFRVLISNLVWHTPYTFEIQAVNGVTKSPFPFQHVSVNIITNQAAAPSIVI 357	
Qy	442	MHQSRTVDSITLWSQDPDQNGVILYELQYKEKSELSEYNATAIKSPNTVTVOGLKAG 501	
Db	358	MHVKATMKSITLWSQDPDQNGVILYELQYKEKSELSEYNATAIKSPNTVTVOGLKAG 417	
Qy	502	AIYVFOVARTVAGYGRYSGMYFOTWTEAYQTSIOEKLPIITGSSAAGLVFLIAVVI 561	
Db	418	VVVVVQVARTVAGYGRYSGMYFOTWTEAYQTSIOEKLPIITGSSAAGLVFLIAVVI 477	
Qy	562	AIVCNRGFERADSEYTDKLQHYTSGHMTPGMKIYIDPFYEDPNEAVRFAKEIDISCV 621	
Db	478	SIVCSRKRTYSKEAVYSDKLQHYTSGRSGPMKIYIDPFYEDPNEAVRFAKEIDISCV 537	
Qy	622	KIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKLKGYTEKQRDFLSEASIMQFDPHN 681	
Db	538	KIEVIGAGEFGEVYKRLKLPGRKEISVAIKLKGYTEKQRDFLSEASIMQFDPHN 597	
Qy	682	VIHLEGVTKSTPMIITFENSGSLDFLRNDQGTIVQLVCMRGIAGMKYLADMN 741	
Db	598	IIRLEGVTKSTPMIITFENSGSLDFLRNDQGTIVQLVCMRGIAGMKYLADMN 657	
Qy	742	VVHRDLARNILVNSLVCKVSDFLGRFLRDEDDTSDPTYSALGKPIRWTAPETAOYR 801	
Db	658	VVHRDLARNILVNSLVCKVSDFLGRFLRDEDDTSDPTYSALGKPIRWTAPETAOYR 717	
Qy	802	KFTSASDWSYGIYVMEVMSYGERPYWDMTNQDVINAIEQDYRLPPPPMDPCPSALHQLMLD 861	
Db	718	KFTSASDWSYGIYVMEVMSYGERPYWDMSNQDVINAIEQDYRLPPPPMDPCPSALHQLMLD 777	
Qy	862	CWQKDRNHRPKFGQIVNTLDKMIINPNLSKMAPLSSGINLPLLDRIIDPTYSNTVDW 921	
Db	778	CWQKDRNHRPKFGQIVNTLDKMIINPNLSKMAPLSSGINLPLLDRIIDPTYSNTVDW 837	

Qy 922 LEAKMGQYKESFANAGFTSFVVVSQMMEDILRLGVLTVLAGHOKKILNSIQVMAQMNQ 980  
Db 838 LSAIKMGQYRDNFLSGFTSLHVVAQVMTSEDLIRIGITLAGHOKKILNSIQVMAQMNQ 896

## RESULT 23

Q6NRE9 PRELIMINARY; PRT; 974 AA.  
ID Q6NRE9  
AC Q6NRE9; T-EMBLrel. 27, Created  
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Oocytes;  
MSDL=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,  
Diatchenko L., Marusica K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzyszewski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Oocytes;  
MSDL=22341132; PubMed=12454917;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
Richardson P.;  
"Genetic and genomic tools for Xenopus research: The NIH Xenopus  
initiative";  
Dev. Dyn. 225:384-391(2002).  
[3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Oocytes;  
Klein S., Strausberg R.;  
Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
tyrosine phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
receptor subfamily.  
DR EMBL; BC070804; AAH70804.1; .  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001090; Ephrin\_receptor.  
DR InterPro; IPR003962; Fhrl1\_subd.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR008979; Gal bind like.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001660; SAM.  
DR InterPro; IPR011510; SAM\_2.



```

DR InterPro; IPR010993; SAM homology.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR001426; Ykase_receptorV.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3_2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM_1; 1.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; EPH_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS00105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Hypothetical protein; Kinase;
KW Phosphorylation; Receptor; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
SQ SEQUENCE 974 AA; 108118 MW; D6634FB63C390F12 CRC64;

Query Match 67.38; Score 3489; DB 2; Length 974;
Best Local Similarity 66.48; Pred. No. 2e-209;
Matches 649; Conservative 144; Mismatches 173; Indels 12; Gaps 5;

Qy 10 LLLPLLAABEETLMDSTTAAELGWMVHPSPGWEVSGYDENNTIRTYQVCNVPSSQ 69
Dy 8 ILALSVAQGLEETLMDTKWTTSELAWAYPDGWEVSGYDEASNPRTTYQCNVLDSNQ 67

Qy 70 NNWLRTFIRRGARHIVHEMFKPSVRDCSSIPSPGCKETFNLYYYEADPSATKTFPN 129
Dy 68 NNWLRTQFIPQDVQVRYVELKFTVRDCNSLPNTPGCKETFNFFYTESDSASADSPF 127

Qy 130 WMENPWKVDITADESPQVDLGRVMKINTEVRSFGPVSRSGFYLAFOYDYGCMSLIA 189
Dy 128 WMENPYIKVDITADESPSRDAG----RVNKLRSFGPLSRGTGYLAFOQLGACVSLIS 183

Qy 190 VRVYRKCPIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGWLV 249
Dy 184 VRVFFKCPQTIAGFASFPETITGAETPSLVIAPGTCVPALEVSVPKLYCNGDGWV 243

Qy 250 PIGCMCKAGFEAVENGTVCRGCSPTFKANQGBEACTHCPINRSTTSEGATNCVCNGY 309
Dy 244 PVGACTCAAGFEPAEKDTQCAACKRGTYKSKQSGSCMPCPINSRAISSAATICSQNGY 303

Qy 310 YRADLDPLDMPCTTIPSAPOAVISVNETSLMLTWTTPRDSGREDLVYNIICKSCSGR 369
Dy 304 YRAGESAETACTSPGAPRHIVSNVNETSVLLEWAPGHGGRGDILYNVICKC--LE 361

Qy 370 GACTRCGDNVQYAPQLGLTEPRYIISDLAHTQYTFEIQAVNGVTPQSPSPQFASVNI 429
Dy 362 RLCSKCGDNVQFWPRLQGLTVQRLVSVHLQAHTKYFSEIQAVNGVSGKSPHIPNYITVNI 421

Qy 430 TTNOAASVNSIMQVSRVDSITLSWSQPOQPNQVILDELOYEYKELSEYNATAIKSP 489
Dy 422 TTNOAASVPMVQSHGSSANSLTSLWAPPSPNGIILDEIKYAKHSGAGNT-VTSQ 480

Qy 490 TNTVQGLKAGAVYVFOVRTARTVAGYGRYSGKMYFOTMTAEYQTSTQEKPLIIGSSA 549
Dy 481 RTTVRMEEMTPTVYVVOVRTARTVAGYGAISEPREFQTIAEDGDRSSIQEQVPMVGSVT 540

Qy 550 AGLVFLIAVVIAIVC-NRRGFERADSEYTKLOHYTSGHMTGPKMKIYIDPFTYEDPNEA 608

Db 541 AGLIFIAVVIIIVCFSRKQRNDSESEYTKLQY---MVPGTCLYIDPFTYEDPNEA 536
Qy 609 VREPAKEIDISCVKIPIQVIGAGEFGVCSGHLKLPGRKREIFVAIKTLKSGYTEKQRDEL 668
Dy 597 VRDFAKEIDISSVKIEBEVIGAGEFGVCRGLKQAGRREQLVAIKTLKAGYTEQQRDEL 656
Qy 669 SEASIMQGFDPHNVHLEGVVTKSTPVMITTEFMENGLSDSLFRQNDGQFTVTLQVGMRL 728
Dy 657 GEASIMQGFDPHNIIRLEGVVTFSRPVMIITEFMENGALDSLFRMNDGQFTVTLQVGLR 716
Qy 729 GIAAGMKYLADMYVHRDLAARNILVSNLVCKVSDFGLSRFLEDDTDPYTSALGGKI 788
Dy 717 GIASGMKYLSEMYVHRDLAARNILVSNLVCKVSDFGLSRFLENSRSDPYTSALGGKI 776
Qy 789 PIRWTAPEALQYRKFTSASDVMSYGIWMVMSYGERPYWDMTNQDVINAIEDYRLPPP 848
Dy 777 PIRWTAPEALSYRKFTSASDVMSYGIWMVMSYGERPYWDMNSQDVINAIEDYRLPPP 836
Qy 849 MDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMRPNPNSLKAMAPLSSGINLPLDRT 908
Dy 837 MDCPSALHQLMLDCWLRDRNLKPKFSQIYSSLDKLRNAASLKVTSFGQAGVSQLDRT 896
Qy 909 IPDYTSFNTVDWELEAIKMGQYKESFANAGFTSFVVSOMMEDILRLGVTLAGHOKKIL 968
Dy 897 VPDYTTFTPTVSDWELEAIKMGQYQENFLSAGFTSFHLVAQWTAEDLLRIGVTLAGHOKKIL 956
Qy 969 NSIQVMRAQNMNQISQVEV 986
Dy 957 NSVQDMRLQMSQTLPVQV 974

RESULT 24
AAH70804 PRELIMINARY; PRT; 974 AA.
AC AAH70804;
DT 13-MAY-2004 (TrEMBLrel. 27, Created)
DT 13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22382257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

```









		759	VCKVSDPGLSRFLEDDTSDPTYSALCGKPIRWTAPEAIQYRKFTSASDVWSYGIVMVE	811
Dg		711	VCKVSDPGLSRFLEDDTSDPTYSALCGKPIRWTAPEAIQYRKFTSASDVWSYGIVMVE	770
Qy		819	VMSYGERPVDMTNODVINAEQDYRLPPPMDCPSALHQLMLDLCWOKRNRHKFGQIVN	878
Dd		771	VMSYGEQPWNNSNODDINAVEQDYRLPPPMDCPSALHQLMLDLCWOKRNRHKFGQIVN	830
Qy		879	TLDKMRNPNSLKAMAPLSSGINIPLLDRITPDVTSTNTVDLMELAKMGQYKESFNAG	938
Dd		831	TLDKLIRNAASLKVTASPSCGMSQPLDLRTVPDYTTTCGDWLDAIKMRYKESFVGAG	890
Qy		939	FTSFDVVSOMMEDILRGVLTLGHOKKILNSIQVMRAQNQTQSVEV	986
Dd		891	PASFDFVAQMATAEDLRIGLVTLGVHGQQKILCSIQDMRLQNMOTLPVOV	938

RESULT 28  
EPB5\_CHICK STANDARD; PRT; 1002 AA.

```

AC Q07497;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-B receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase CEK9).
DN Name=CEK9; Synonyms=CEK9;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
[2]
SEQUENCE FROM N.A.
RP MEDLINE=97066069; PubMed=8909550;
RA Soans C., Holash J.A., Pavlova Y., Pasquale E.B.;
RT "Developmental expression and distinctive tyrosine phosphorylation of the Eph-related receptor tyrosine kinase Cek9.";
RI J. Cell Biol. 135:781-795(1996).
```

(2)  
PARTIAL SEQUENCE FROM N.A.  
RP MEDLINE=93288394; PubMed=8510926;  
RA Sajjadi F.G., Pasquale E.B.;  
RT "Five novel avian Eph-related tyrosine kinases are differentially expressed.";  
RI Oncogene 8:1807-1813(1993).  
CC -!- FUNCTION: Receptor for members of the ephrin-B family.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Most abundant in thymus and detectable in brain, retina, kidney, lung and heart. Not detected in skeletal muscle and liver.  
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.  
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.

---

This SWIS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement or send an email to license@isb-sib.ch).

---

EMBL; U23783; AAC41054.1; --  
HSP; P54763; LUPA.  
InterPro; IPRO06209; EGF like.  
InterPro; IPRO01090; Ephrin\_receptor.  
InterPro; IPRO03962; FNIII\_subd.  
InterPro; IPRO03961; FN\_III.

DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR008979; Gal\_bind like.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001660; SAM.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_kinase\_AS.  
DR InterPro; IPR001426; Ykase\_receptorV.  
DR Pfam; PF00041; fn3\_2.  
DR Pfam; PF00041; fn3\_2.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00536; SAM; 1.  
DR PRINTS; PR00014; FNTYPEIII.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD001495; Ephrin\_receptor; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00615; EPH\_lbd; 1.  
DR SMART; SM00060; FN3\_2.  
DR SMART; SM00454; SAM; 1.  
DR SMART; SM00219; TyRkc; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS00853; FN3\_2.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR PROSITE; PS00105; SAM\_DOMAIN; 1.  
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;  
KW Transferrase; Transmembrane; Tyrosine-protein kinase.  
FT SIGNAL 1 29 Potential.  
FT CHAIN 30 1002 Ephrin type-B receptor 5.  
FT DOMAIN 30 564 Extracellular (Potential).  
FT TRANSMEM 565 585 Potential.  
FT DOMAIN 586 1002 Cytoplasmic (Potential).  
FT DOMAIN 195 338 Cys-rich.  
FT DOMAIN 342 444 Fibronectin type-III 1.  
FT DOMAIN 454 545 Fibronectin type-III 2.  
FT DOMAIN 637 900 Protein kinase.  
FT DOMAIN 862 865 Poly-Pro.  
FT DOMAIN 929 993 SAM.  
FT SITE 1000 1002 PDZ-binding motif (Potential).  
FT NP\_BIND 643 651 ATP (By similarity).  
FT BINDING 669 669 ATP (By similarity).  
FT ACT\_SITE 762 762 By similarity.  
FT MOD\_RES 612 612 Phosphotyrosine (by autocatalysis) (Potential).  
FT MOD\_RES 618 618 Phosphotyrosine (by autocatalysis) (Potential).  
FT MOD\_RES 796 796 Phosphotyrosine (by autocatalysis) (Potential).  
FT MOD\_RES 946 946 Phosphotyrosine (by autocatalysis) (Potential).  
FT CARBOHYD 446 446 N-linked (GlcNAc...) (Potential).  
FT SEQUENCE 1002 AA; 111947 MW; 6D9635B500D8B0DA CRC64;  
Query Match 64.7%; Score 3354.5; DB 1; Length 1002;  
Best Local Similarity 63.0%; Pred. No. 5.4e-201;  
Matches 618; Conservative 152; Mismatches 198; Indels 13; Gaps 6;  
QY 15 LLAIVETLMDSTATLAELGMVHPSPGWEVSGYDENMTIRTYQVNVFSSQNNWLR 74  
DB 26 LVTSLEILLDTTGETSEIGTSHPPDGWEVSRDDKERQINTFQVCNNDEPQNNWLR 85  
QY 75 TKIRRRGARIHVEMKFSVRDCCSIPSVGSKETENLYYADPDSAKTFPNWNP 134  
DB 86 THPIERGARRHVRLHFSVRDCASMRVASTCKETFLYHQSDVDVDSQELPEVHEGP 145  
QY 135 WKVVDITAADESFSQVDLGRVWVKINTEVRSFGVSRSGFYLAQDYGGCMSLIAVRVY 194  
DB 146 WTKVDITAADESFSQVDRTGKVRVMVKSFGPLTKHGYLAQDSGACMSLVAVQVFF 205  
QY 195 RKPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVP----IKLYCNGDGEWLVP 250

Db 206 YKCPAVVKGFPASPFPETPAGGERTSLVESLGTCTVANAEEASTSGSGVRLHNCGEWMVA 265  
QY 251 IGRCMCKAGFEAVENGTVCRGCPGFPKANQGBEACTHCIPNSRT--TSEGATVCVCRNG 308  
Db 266 TGRCSCKAGYQVDNEQACQACPIGSKASVGDDPCLLCPAHSAPLPLPGSEICVCQSH 325  
QY 309 YIRADLDPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGREDLVNIIICKSGS- 367  
Db 326 YIRSASDNSDAPCTGTPSAPRDLSEIVGSNVLWTWRLPKDLGRKDVFNVICKECPTR 385  
QY 368 GRGACTRCGDNVQYAPROLGLTEPRYIYISLLAHTQYTFEIOAVNGVTDOSPSPQASV 427  
Db 386 SAGTCVRCGDNVQFBPRQVGLTESRVQVSNLLARVQYTFEIOAVNLVTELSEAPQATI 445  
QY 428 NITNQAAPSASVIMHGVSRVDSITLWSQPPQPNVILDYELQVYVEKELSEYNATAIK 487  
Db 446 NVSTQSQVPSAIPMMHGVSRVDSITLWSQPPQPNVILDYELQVYVEKELSEYNATAIK 505  
QY 488 SPTNTVTVOGLKAGAIYVFOVARTVAGYGRYSGKMYFQMTTAEYQTSIQEKLPLIGS 547  
Db 506 SETNMTILNLSPGKIYVFOVARTVAGYGRYSGKMYFQMTTAEYQTSIQEKLPLIGS 565  
QY 548 SAAGLVFLI--AVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTQMKIYIDPFTYEDP 605  
Db 566 ALGGLAFLVIAAIIAIIIPKSK---RRETPYTDRLQYISTRGL-GVKYIYIDPSTYEDP 621  
QY 606 NEAVRFAKEIDISCVKIEOVIGAGFEGVCSGHLKPGKREIFVAIKTLKSGVTEKQRR 665  
Db 622 NEAIRFAKEIDVSTFKIEVIGSGFEGVCFGRLKHPRKREYTVALKTLKSGVTEKQRR 681  
QY 666 DFLSEASIMGQFDPHPVHLEGVVTKSTPYMIITEFMENGLSDSLRQNDGQFTVIQLVG 725  
Db 682 EFLSEASIMGQFDPHPVHLEGVVTKSRPVMIVTEFMENGLSDSLRQNDGQFTVIQLVG 741  
QY 726 MLRGIAAGKYLADMYVHRDLAARNILVNSLVCKYVDSFGLSRFLEDDTSDPTYSALG 785  
Db 742 MLRGIAAGKRYLSDMYVHRDLAARNILVNSLVCKYVDSFGLSRFLEDDTSDPTYSALG 801  
QY 786 GKPIPIWTAPETAIQYRKFTSASDVWSYGVIMVWVMSYGERPYWDMTQDVNATIEQDYL 845  
Db 802 CKPIPIWTAPETAIQYRKFTSSDVWSYGVIMVWVMSYGERPYWDMTQDVNATIEQDYL 861  
QY 846 PPMDCPSALHQLMDCQKDRNHRPKFGQIVNTLDMIRNPNLSLKAMAPLSSGINLPL 905  
Db 862 PPPDCPTVLHLLMDCQKDRVQRPKEQIVSALDKMIRKPSALKATGTSRSPQPLL 921  
QY 906 DRTIPDYTFNTVDWELAIKMQYKESFANAGFTSFDVVSQMMEDILGLVTLGHQK 965  
Db 922 SNSPPDPFPLSNAHEWLDKMGRYKENFDQAGLITFDVISRMTLEDLQIGITLVGHQK 981  
QY 966 KILNSIQVMRAQMNQIQSVEV 986  
Db 982 KILNSIQVMRAQMNQIQSVEV 1002

RESULT 29  
Q90ZN8 PRELIMINARY; PRT; 923 AA.  
AC Q90ZN8;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Eph\_receptor\_Eph3.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94200158; PubMed=8149909;  
RA Xu Q., Holder N., Patient R., Wilson S.W.;





Search completed: December 30, 2004, 16:49:57  
Job time : 221 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 16:43:36 ; Search time 157 Seconds  
(without alignments)  
2259.182 Million cell updates/sec

Title: US-09-914-883-2

Perfect score: 5188

Sequence: 1 MALRRIGALLLLPLLAIVE.....ILNSIQVMRAQMNIQSVEV 986

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5181	99.9	1055	16	US-10-648-593-139
2	5181	99.9	1055	17	US-10-757-262-100
3	5181	99.9	1055	17	US-10-768-158-8
4	5171.5	99.7	987	14	US-10-295-027-1193
5	4993.5	96.3	995	15	US-10-029-020-62
6	3934.5	75.8	984	15	US-10-029-020-60
7	3670.5	70.7	998	14	US-10-295-027-1183
8	3670.5	70.7	998	17	US-10-783-528-112
9	3661.5	70.6	998	14	US-10-354-358-4
10	3661.5	70.6	998	17	US-10-723-860-2850
11	3661.5	70.6	1007	15	US-10-276-774-2273
12	3603.5	69.5	993	14	US-10-187-958-1
13	3594.5	69.3	896	16	US-10-408-765A-2942
14					Sequence 139, App
15					Sequence 100, App
16					Sequence 8, Appli
17					Sequence 119, Ap
18					Sequence 62, Appl
19					Sequence 60, Appl
20					Sequence 1183, Ap
21					Sequence 112, App
22					Sequence 4, Appli
23					Sequence 2850, Ap
24					Sequence 2273, Ap
25					Sequence 1, Appli

14	3075.5	59.3	985	15	US-10-029-020-61	Sequence 61, Appl
15	3053	58.8	991	10	US-09-823-187-44	Sequence 44, Appl
16	3048	58.8	953	14	US-10-412-277-7	Sequence 7, Appli
17	3045	58.7	986	17	US-10-723-860-597	Sequence 597, App
18	3038.5	58.6	993	10	US-09-823-187-39	Sequence 39, Appl
19	3038.5	58.6	993	10	US-09-823-187-41	Sequence 41, Appl
20	3038	58.6	1104	9	US-09-982-610-36	Sequence 36, Appl
21	3036	58.5	1037	14	US-10-316-124-3	Sequence 3, Appli
22	3036	58.5	1037	14	US-10-353-690-40	Sequence 40, Appl
23	3031	58.4	975	14	US-10-412-277-8	Sequence 8, Appli
24	3028	58.4	998	10	US-09-823-187-40	Sequence 40, Appl
25	3013	58.1	998	10	US-09-823-187-42	Sequence 42, Appl
26	3013	58.1	998	10	US-09-823-187-43	Sequence 43, Appl
27	2930.5	56.5	983	9	US-09-771-161A-227	Sequence 227, App
28	2930.5	56.5	983	14	US-10-205-823-97	Sequence 97, Appl
29	2930.5	56.5	983	14	US-10-345-680-2	Sequence 2, Appli
30	2930.5	56.5	983	14	US-10-295-027-602	Sequence 602, App
31	2930.5	56.5	983	15	US-10-029-020-59	Sequence 59, Appl
32	2928	56.4	968	14	US-10-412-277-6	Sequence 6, Appli
33	2923	56.3	1005	15	US-10-029-020-63	Sequence 63, Appl
34	2844	54.8	1276	9	US-09-982-610-24	Sequence 24, Appl
35	2838	54.7	1036	14	US-10-220-955-21	Sequence 21, Appl
36	2835	54.6	1036	10	US-09-971-708-2	Sequence 2, Appli
37	2835	54.6	1036	14	US-10-245-752-104	Sequence 104, App
38	2835	54.6	1036	14	US-10-245-859-104	Sequence 104, App
39	2835	54.6	1036	14	US-10-245-103-104	Sequence 104, App
40	2835	54.6	1036	14	US-10-245-107-104	Sequence 104, App
41	2835	54.6	1036	14	US-10-245-143-104	Sequence 104, App
42	2835	54.6	1036	14	US-10-245-771-104	Sequence 104, App
43	2835	54.6	1036	14	US-10-245-851-104	Sequence 104, App
44	2835	54.6	1036	14	US-10-245-883-104	Sequence 104, App
45	2835	54.6	1036	14	US-10-237-535-104	Sequence 104, App
46	2835	54.6	1036	14	US-10-238-183-104	Sequence 104, App
47	2835	54.6	1036	14	US-10-238-283-104	Sequence 104, App
48	2835	54.6	1036	14	US-10-238-370-104	Sequence 104, App
49	2835	54.6	1036	14	US-10-245-055-104	Sequence 104, App
50	2835	54.6	1036	14	US-10-245-147-104	Sequence 104, App
51	2835	54.6	1036	14	US-10-245-730-104	Sequence 104, App
52	2835	54.6	1036	14	US-10-245-739-104	Sequence 104, App
53	2835	54.6	1036	14	US-10-246-210-104	Sequence 104, App
54	2835	54.6	1036	14	US-10-239-196-104	Sequence 104, App
55	2835	54.6	1036	14	US-10-243-024-104	Sequence 104, App
56	2835	54.6	1036	14	US-10-243-409-104	Sequence 104, App
57	2835	54.6	1036	14	US-10-245-621-104	Sequence 104, App
58	2835	54.6	1036	14	US-10-245-880-104	Sequence 104, App
59	2835	54.6	1036	14	US-10-245-033-104	Sequence 104, App
60	2835	54.6	1036	14	US-10-243-095-104	Sequence 104, App
61	2835	54.6	1036	14	US-10-245-185-104	Sequence 104, App
62	2835	54.6	1036	14	US-10-245-427-104	Sequence 104, App
63	2835	54.6	1036	14	US-10-245-473-104	Sequence 104, App
64	2835	54.6	1036	14	US-10-245-770-104	Sequence 104, App
65	2835	54.6	1036	14	US-10-245-877-104	Sequence 104, App
66	2835	54.6	1036	14	US-10-246-976-104	Sequence 104, App
67	2835	54.6	1036	14	US-10-243-320-104	Sequence 104, App
68	2835	54.6	1036	14	US-10-242-743-104	Sequence 104, App
69	2835	54.6	1036	14	US-10-242-845-104	Sequence 104, App
70	2835	54.6	1036	14	US-10-237-636-104	Sequence 104, App
71	2835	54.6	1036	14	US-10-238-325-104	Sequence 104, App
72	2835	54.6	1036	14	US-10-238-346-104	Sequence 104, App
73	2835	54.6	1036	14	US-10-238-411-104	Sequence 104, App
74	2835	54.6	1036	14	US-10-243-124-104	Sequence 104, App
75	2835	54.6	1036	14	US-10-243-425-104	Sequence 104, App
76	2835	54.6	1036	14	US-10-243-446-104	Sequence 104, App
77	2835	54.6	1036	14	US-10-245-874-104	Sequence 104, App
78	2835	54.6	1036	14	US-10-242-653-104	Sequence 104, App
79	2835	54.6	1036	14	US-10-243-167-104	Sequence 104, App
80	2835	54.6	1036	14	US-10-243-388-104	Sequence 104, App
81	2835	54.6	1036	14	US-10-244-947-104	Sequence 104, App
82	2835	54.6	1036	14	US-10-244-968-104	Sequence 104, App
83	2835	54.6	1036	14	US-10-244-990-104	Sequence 104, App
84	2835	54.6	1036	14	US-10-245-079-104	Sequence 104, App
85	2835	54.6	1036	14	US-10-245-127-104	Sequence 104, App
86	2835	54.6	1036	14	US-10-245-207-104	Sequence 104, App

87 2835 54.6 1036 14 US-10-245-646-104 Sequence 104, App  
88 2835 54.6 1036 14 US-10-245-695-104 Sequence 104, App  
89 2835 54.6 1036 14 US-10-245-699-104 Sequence 104, App  
90 2835 54.6 1036 14 US-10-245-737-104 Sequence 104, App  
91 2835 54.6 1036 14 US-10-245-878-104 Sequence 104, App  
92 2835 54.6 1036 14 US-10-245-890-104 Sequence 104, App  
93 2835 54.6 1036 14 US-10-245-899-104 Sequence 104, App  
94 2835 54.6 1036 14 US-10-245-900-104 Sequence 104, App  
95 2835 54.6 1036 14 US-10-247-058-104 Sequence 104, App  
96 2835 54.6 1036 14 US-10-245-454-104 Sequence 104, App  
97 2835 54.6 1036 14 US-10-237-471-104 Sequence 104, App  
98 2835 54.6 1036 14 US-10-238-261-104 Sequence 104, App  
99 2835 54.6 1036 14 US-10-238-324-104 Sequence 104, App  
100 2835 54.6 1036 14 US-10-241-860-104 Sequence 104, App

ALIGNMENTS

RESULT 1  
US-10-648-593-139  
; Sequence 139, Application US/10648593  
; Publication No. US20040106132A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT  
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
; FILE REFERENCE: D0273 NP  
; CURRENT APPLICATION NUMBER: US/10/648,593  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 60/406,385  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 557  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 139  
; LENGTH: 1055  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-593-139

Query Match 99.9%; Score 5181; DB 16; Length 1055;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALRRGAAALLLLPAAVEETLMDSTTATAEIGCMVHPSPGSEVSGYDENMNTIYQ 60  
Db 1 MALRRGAAALLLLPAAVEETLMDSTTATAEIGCMVHPSPGSEVSGYDENMNTIYQ 60  
Qy 61 VCNVFESSONNLTKFIRRRGAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 120  
Db 61 VCNVFESSONNLTKFIRRRGAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADF 120  
Qy 121 DSATKTFNNMNMWPKVDTTAADESPQVLDGRVKMINTEVRSFGPVSRSGLYAFQD 180  
Db 121 DSATKTFNNMNMWPKVDTTAADESPQVLDGRVKMINTEVRSFGPVSRSGLYAFQD 180  
Qy 181 YGGCNSLIANVFRKCPRIIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
Db 181 YGGCNSLIANVFRKCPRIIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLY 240  
Qy 241 CNGDGEWLVPICRCMKAGFAVENGTVCRCPSGTTFKANQDEACTHCPINSRTTSEGA 300  
Db 241 CNGDGEWLVPICRCMKAGFAVENGTVCRCPSGTTFKANQDEACTHCPINSRTTSEGA 300  
Qy 301 TNCVCRNGYYRADLDPLDMPCTTIPSPAPQAVISSVNETSLMLEWTPPRDSGGRDLVYNI 360  
Db 301 TNCVCRNGYYRADLDPLDMPCTTIPSPAPQAVISSVNETSLMLEWTPPRDSGGRDLVYNI 360  
Qy 361 ICKSCGSGRGACTRCGDNVQVAPROUGLTPRIYISDLAHTQYTFEIQAVNGVTDQSPF 420  
Db 361 ICKSCGSGRGACTRCGDNVQVAPROUGLTPRIYISDLAHTQYTFEIQAVNGVTDQSPF 420

Qy 421 SPQFASVNTITNQAAAPSVAIVHQSRTVDSITLWSQDPQDPNGVILDYELQYKEKELSE 480  
Db 421 SPQFASVNTITNQAAAPSVAIVHQSRTVDSITLWSQDPQDPNGVILDYELQYKEKELSE 480  
Qy 481 YNATAIKSPNTVTVOGLKAGAIYVQVRARVAGYGRYSGWYFQTMTEAYQTSIQBK 540  
Db 481 YNATAIKSPNTVTVOGLKAGAIYVQVRARVAGYGRYSGWYFQTMTEAYQTSIQBK 540  
Qy 541 LPLITGSSAAGLAVFLIAVVAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600  
Db 541 LPLITGSSAAGLAVFLIAVVAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600  
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660  
Db 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT 660  
Qy 661 EKQRDFLSEASIMGQFDHPNVHLEGVVTKSTPVMITEFNGENGLDSFLRQNDQOFTV 720  
Db 661 EKQRDFLSEASIMGQFDHPNVHLEGVVTKSTPVMITEFNGENGLDSFLRQNDQOFTV 720  
Qy 721 IQLVGMRLGIAAGMKYLADNMVYHRDLAARNILVNSNLVCKYDFGLSRFLEDDTSDPTY 780  
Db 721 IQLVGMRLGIAAGMKYLADNMVYHRDLAARNILVNSNLVCKYDFGLSRFLEDDTSDPTY 780  
Qy 781 TSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGVIMVMEVMSYGERPYDMTNDQVINAIE 840  
Db 781 TSALGGKIPIRWTAPEAIQYRKFTSASDVMSYGVIMVMEVMSYGERPYDMTNDQVINAIE 840  
Qy 841 QDYRLPPMDPCPSALHOLMDCWQKDRNHRPFGQIVNTLDKMRNPNSLKAWAPLSSGI 900  
Db 841 QDYRLPPMDPCPSALHOLMDCWQKDRNHRPFGQIVNTLDKMRNPNSLKAWAPLSSGI 900  
Qy 901 NLPLDRTTIPDYSFNTVDWELEAIKMGQYKESFANAGTSPDVVSQMMEDILRLGVTL 960  
Db 901 NLPLDRTTIPDYSFNTVDWELEAIKMGQYKESFANAGTSPDVVSQMMEDILRLGVTL 960  
Qy 961 AGHQKILNSIQVMRAQMNQIOSVE 985  
Db 961 AGHQKILNSIQVMRAQMNQIOSVE 985  
RESULT 2  
US-10-757-262-100  
; Sequence 100, Application US/10757262  
; Publication No. US20040197825A1  
; GENERAL INFORMATION:  
; APPLICANT: Karicheti, Venkateswarlu  
; APPLICANT: Eliasof, Scott D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,  
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,  
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,  
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 2245, 2387, 52908, 69112, 14990,  
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,  
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,  
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,  
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR  
; FILE OF INVENTION: 55053  
; FILE REFERENCE: MEI03-007PIRNONMIN  
; CURRENT APPLICATION NUMBER: US/10/757,262  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US 60/440,318  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/444,783  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/457,901  
; PRIOR FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/468,775  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/471,614  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US 60/478,742

```
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-100

Query Match      99.9%; Score 5181; DB 17; Length 1055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MALRRLGAALLLLP LLA AVEETLMDSTTATAELGWMVHPSPSGWEVSGYDENMNTIRTYQ 60
Db      1  MALRRLGAALLLLP LLA AVEETLMDSTTATAELGWMVHPSPSGWEVSGYDENMNTIRTYQ 60

Qy      61  VCNVFESSQNNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADF 120
Db      61  VCNVFESSQNNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADF 120

Qy      121  DSATKTFPNMNMENPWKVDITIAADESFQVDLGRVNMKINTEVRSFQVSRSGFYLAQD 180
Db      121  DSATKTFPNMNMENPWKVDITIAADESFQVDLGRVNMKINTEVRSFQVSRSGFYLAQD 180

Qy      181  YGGCMSLIAVRVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLY 240
Db      181  YGGCMSLIAVRVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLY 240

Qy      241  CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSGTTFKANGDDEACTHCPINSRTTSEGA 300
Db      241  CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSGTTFKANGDDEACTHCPINSRTTSEGA 300

Qy      301  TNCVCRNGYRADLDPLDMCTTTPSAPOAVISSNETSLMLEWTPPRDSGGREDLYVNI 360
Db      301  TNCVCRNGYRADLDPLDMCTTTPSAPOAVISSNETSLMLEWTPPRDSGGREDLYVNI 360

Qy      361  ICKSCSGRGACTRCGDNVOYAPQLGLTEPRIIYISDLAHTQYTFEIQAVNGVTDQSPF 420
Db      361  ICKSCSGRGACTRCGDNVOYAPQLGLTEPRIIYISDLAHTQYTFEIQAVNGVTDQSPF 420

Qy      421  SPQFASVNIITNQAPSASVIMHQVSRVDSITLSWSQDPQNGVILDYELQYYEKELSE 480
Db      421  SPQFASVNIITNQAPSASVIMHQVSRVDSITLSWSQDPQNGVILDYELQYYEKELSE 480

Qy      481  YNATAIKSPNTVTVOGLKAGAIYVFOURARTVAGYGRYSGKMYFQMTAEYQTSIQEK 540
Db      481  YNATAIKSPNTVTVOGLKAGAIYVFOURARTVAGYGRYSGKMYFQMTAEYQTSIQEK 540

Qy      541  LPLIIGSSAAGLVFLIAVWVAIVCNRRGPERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600
Db      541  LPLIIGSSAAGLVFLIAVWVAIVCNRRGPERADSEYTDKLOHYTSGHMTPGMKIYIDPF 600

Qy      601  TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFQVSCVCHLKLPGKREIFVAIKTLKSGYT 660
Db      601  TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFQVSCVCHLKLPGKREIFVAIKTLKSGYT 660

Qy      661  EKQRDFLSEASIMGQDFHPNVHLEGVYKSTPVMIIITEPMENGSLDSFLRQNDGQFTV 720
Db      661  EKQRDFLSEASIMGQDFHPNVHLEGVYKSTPVMIIITEPMENGSLDSFLRQNDGQFTV 720

Qy      721  IQLVGLMRLGTAAGMKYLADNMNVHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPTY 780
Db      721  IQLVGLMRLGTAAGMKYLADNMNVHRDLAARNILVNSNLVCKVSDFGLSRFLDDTSDPTY 780
```

```
RESULT 3
US-10-768-158-8
; Sequence 8, Application US/10768158
; Publication No. US20040204359A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliassof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 16386, 15402, 21165, 1423,
; TITLE OF INVENTION: 636, 12303, 21425, 27410, 38554, 38555, 55063, 57145, 59914,
; TITLE OF INVENTION: 94921, 16852, 33260, 58573, 30911, 85913, 14303, 16816,
; TITLE OF INVENTION: 17827 OR 32620
; FILE REFERENCE: MPI03-012PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/768,158
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,781
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/452,291
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: US 60/454,540
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 60/478,805
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/491,048
; PRIOR FILING DATE: 2003-07-30
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 8
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-768-158-8
```

```
Query Match      99.9%; Score 5181; DB 17; Length 1055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MALRRLGAALLLLP LLA AVEETLMDSTTATAELGWMVHPSPSGWEVSGYDENMNTIRTYQ 60
Db      1  MALRRLGAALLLLP LLA AVEETLMDSTTATAELGWMVHPSPSGWEVSGYDENMNTIRTYQ 60

Qy      61  VCNVFESSQNNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADF 120
Db      61  VCNVFESSQNNWLRTKPIRRRGAHRIHVEMKFSVRDCSSIPSPVSGCKETFNLYYYEADF 120

Qy      121  DSATKTFPNMNMENPWKVDITIAADESFQVDLGRVNMKINTEVRSFQVSRSGFYLAQD 180
Db      121  DSATKTFPNMNMENPWKVDITIAADESFQVDLGRVNMKINTEVRSFQVSRSGFYLAQD 180

Qy      181  YGGCMSLIAVRVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLY 240
Db      181  YGGCMSLIAVRVFRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLY 240

Qy      241  CNGDGEWLVPIGRCMCKAGFEAVENGTVCRGCPSGTTFKANGDDEACTHCPINSRTTSEGA 300
```

```

1  PRIOR FILING DATE: 2000-09-15
2  PRIOR APPLICATION NUMBER: US 60/350,666
3  PRIOR FILING DATE: 2001-11-13
4  PRIOR APPLICATION NUMBER: US 60/335,394
5  PRIOR FILING DATE: 2001-11-15
6  PRIOR APPLICATION NUMBER: US 60/332,464
7  PRIOR FILING DATE: 2001-11-21
8  PRIOR APPLICATION NUMBER: US 60/334,393
9  PRIOR FILING DATE: 2001-11-29
10 PRIOR APPLICATION NUMBER: US 60/340,376
11 PRIOR FILING DATE: 2001-12-14
12 PRIOR APPLICATION NUMBER: US 60/347,211
13 PRIOR FILING DATE: 2002-01-08
14 PRIOR APPLICATION NUMBER: US 60/347,349
15 PRIOR FILING DATE: 2002-01-10
16 PRIOR APPLICATION NUMBER: US 60/355,250
17 PRIOR FILING DATE: 2002-02-08
18 PRIOR APPLICATION NUMBER: US 60/356,714
19 PRIOR FILING DATE: 2002-02-13
20 Remaining Prior Application data removed - See File Wrapper or PALM.
21 NUMBER OF SEQ ID NOS: 1386
22 SOFTWARE: PatentIn Ver. 2.1
23 SEQ ID NO 1193
24 LENGTH: 987
25 TYPE: PRT
26 ORGANISM: Homo sapiens
27 US-10-295-027-1193

```

Query Match	99.7%;	Score 5171.5;	DB 14;	Length 987;
Best Local Similarity	99.7%;	Pred. Num. 0;		
Matches 984;	Conservative	2;	Mismatches 0;	Indels 1; Gaps 1;
QY	1	MALRRLGAAALLLPL	LAAVEETLMDSTTATAELGWMVHP	PGSWEVSGYDENMNTIRYQ 60
DB	1	MALRRLGAAALLLPL	LAAVEETLMDSTTATAELGWMVHP	PGSWEVSGYDENMNTIRYQ 60
QY	61	VCNVFESSQNWLRTKPI	RRRGHRIHVEMKESVDRDCSSI	PSVPSCKETNLXYEADF 120
DB	61	VCNVFESSQNWLRTKPI	RRRGHRIHVEMKESVDRDCSSI	PSVPSCKETNLXYEADF 120
QY	121	DSATKTPFNWMEPNWKVD	TIAADESFSQVDLGGRVKMKINT	EVRSFGVPSRSGVFLAQD 180
DB	121	DSATKTPFNWMEPNWKVD	TIAADESFSQVDLGGRVKMKINT	EVRSFGVPSRSGVFLAQD 180
QY	181	YGGCMSLIAVRVYRKCP	RIIIONGAIFQETLSGABSTSL	VAARGSCIANAEVDVPKILY 240
DB	181	YGGCMSLIAVRVYRKCP	RIIIONGAIFQETLSGABSTSL	VAARGSCIANAEVDVPKILY 240
QY	241	CNGDEWLVP	IGRCMKKAGFEAVENGTV	CRGCPSTGTFKANQGDCACTHCPINSRTTSSGA 300
DB	241	CNGDEWLVP	IGRCMKKAGFEAVENGTV	CRGCPSTGTFKANQGDCACTHCPINSRTTSSGA 300
QY	301	TNCVCRNGYRADLDPL	DMCTTIPSAQAVISSVNNETSL	MLEWTPPRDSGGREDLVYNI 360
DB	301	TNCVCRNGYRADLDPL	DMCTTIPSAQAVISSVNNETSL	MLEWTPPRDSGGREDLVYNI 360
QY	361	ICKSCSGRGACTRCG	DNVOYAPRQLGTEBPRIYI	SDLLAHTQYFETIOAVNGVTDQSPF 420
DB	361	ICKSCSGRGACTRCG	DNVOYAPRQLGTEBPRIYI	SDLLAHTQYFETIOAVNGVTDQSPF 420
QY	421	SPOFASVNITTNQAP	SAVSIMHGVSRVDSITLSWSQ	PDQPNGVILDYELQYVEKEUSE 480
DB	421	SPOFASVNITTNQAP	SAVSIMHGVSRVDSITLSWSQ	PDQPNGVILDYELQYVEKEUSE 480
QY	481	YNATAIKSPTNTVT	VOGLKAGAIYVFOVRARTVAG	YGRYSGKMVFOTMTEAEYQTSIOEK 540
DB	481	YNATAIKSPTNTVT	VOGLKAGAIYVFOVRARTVAG	YGRYSGKMVFOTMTEAEYQTSIOEK 540
QY	541	LPLIITGSSAAGLV	FLIAVWVIAVCN--RRCFERAD	SEYTDKLQHTSGHMTGPMKIYIDP 599
DB	541	LPLIITGSSAAGLV	FLIAVWVIAVCNRRRRR	FERADSEYTDKLQHTSGHMTGPMKIYIDP 600
QY	600	FYVEDPNNAVREFAKE	IDISCVKIEQVIGAFEGEVC	SGHLKPGKRETFVAKTLXSGY 659

[illegible]

Db 601 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGY 660  
Qy 660 TEKORRDFLEASATMGQDFHPNVHLHLEGVTKSTPVMIIITEFWENGSLDSFLRQNDQOFT 719  
Db 661 TEKORRDFLEASATMGQDFHPNVHLHLEGVTKSTPVMIIITEFWENGSLDSFLRQNDQOFT 720  
Qy 720 VIQLVGMRLGIAAGMYKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLBEDDTSDDPT 779  
Db 721 VIQLVGMRLGIAAGMYKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLBEDDTSDDPT 780  
Qy 780 YTSALGKGKIPIRWTAPEAIQYRKFTSASDVNSYGIWVWVMSYGERPYWDMTQDVINAI 839  
Db 781 YTSALGKGKIPIRWTAPEAIQYRKFTSASDVNSYGIWVWVMSYGERPYWDMTQDVINAI 840  
Qy 840 EODYRLPPPPDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSG 899  
Db 841 EODYRLPPPPDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSG 900  
Qy 900 INPLDRTTIPDYTSFNTVDWELEAIKMGQYKESFANAGFTSFVVVSQMMEDIILRLGVT 959  
Db 901 INPLDRTTIPDYTSFNTVDWELEAIKMGQYKESFANAGFTSFVVVSQMMEDIILRVGLT 960  
Qy 960 LAGHQKILNSIQVMRAQMNQIOSVEV 986  
Db 961 LAGHQKILNSIQVMRAQMNQIOSVEV 987

## RESULT 5

US-10-029-020-62  
; Sequence 62, Application US/10029020  
; Publication No. US20040033971A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangolli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/10/029,020  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 60/294,075  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/288,153  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 62  
; LENGTH: 995  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-10-029-020-62

Query Match 96.3%; Score 4993.5; DB 15; Length 995;  
Best Local Similarity 95.8%; Pred. No. 0;  
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;  
Qy 10 LLLPLLAAREETLMDSTATAELGMMVHPSPGEEVSGYDNNMTIRTYQVCNVFESSQ 69  
Db 18 LALLPLLAAREETLMDSTATAELGMMVHPSPGEEVSGYDNNMTIRTYQVCNVFESSQ 77  
Qy 70 NNWLRTKIRRRGAHRIHVEMKFSVRDCSSIPSPVFGSKETFNLYYYEADPDSATKTFPN 129

Db 78 NNWLRTKIRRRGAHRIHVEMKFSVRDCSSIPSPVFGSKETFNLYYYEADPDSATKTFPN 137  
Qy 130 WMENPMVKVDYTIADRSFSQVDLGGVRVMKINTEVRGFPVSRGFFYLAFOYDYGCMSLIA 189  
Db 138 WMENPMVKVDYTIADRSFSQVDLGGVRVMKINTEVRGFPVSRGFFYLAFOYDYGCMSLIA 197  
Qy 190 VRVYRKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 249  
Db 198 VRVYRKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLV 257  
Qy 250 PIGRCMCKAGFEAVENGTVCRGCPSTFKANQDDEACTHCPINSTRTISEGATNCVCNGY 309  
Db 258 PIGRCMCKAGFEAVENGTVCRGCPSTFKASQDDEGCVHCPINSTRTISEGATNCVCNGY 317  
Qy 310 YRADLPLDMPCPTTIPSAQAVISSVNETSLMLEWTTPRDSGGREDLVYNIICKSCSGSR 369  
Db 318 YRADLPLDMPCPTTIPSAQAVISSVNETSLMLEWTTPRDSGGREDLVYNIICKSCSGSR 377  
Qy 370 GACTRCGDNVQYAPRQGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 429  
Db 378 GACTRCGDNVQYAPRQGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNI 437  
Qy 430 TTNQAAPSAVSIHQVSRVTDSITLSWSQDQPNGVILDYELQYVEKELSEYNATAKSP 489  
Db 438 TTNQAAPSAVSIHQVSRVTDSITLSWSQDQPNGVILDYELQYVEKELSEYNATAKSP 497  
Qy 490 TTNVTVOGLKAGAIYVFOVRARTVAGYGRYSGMYFOTMTEAEVQTSIQSKPLIIGSSA 549  
Db 498 TTNVTVOGLKAGAIYVFOVRARTVAGYGRYSGMYFOTMTEAEVQTSIQSKPLIIGSSA 557  
Qy 550 AGLVFLIAVVVIAIVCN-RRGERADSEYTDKLQHYTSGHMTGPKMIYIDPFTYEDPNEA 608  
Db 558 AGLVFLIAVVVIAIVCN-RRGERADSEYTDKLQHYTSGHMTGPKMIYIDPFTYEDPNEA 617  
Qy 609 VRFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFL 668  
Db 618 VRFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFL 677  
Qy 669 SEASIMQDFHPNVHLHLEGVTKSTPVMIIITEFWENGSLDSFLRQNDQOFTVIOLVGMLR 728  
Db 678 SEASIMQDFHPNVHLHLEGVTKSTPVMIIITEFWENGSLDSFLRQNDQOFTVIOLVGMLR 737  
Qy 729 GIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLBEDDTSDDPTYSALGKI 788  
Db 738 GIAAGMKYLADMYVHRDLAARNILVNSNLVCKYSDFGLSRFLBEDDTSDDPTYSALGKI 797  
Qy 789 PIRWTAPEAIQYRKFTSASDVNSYGIWVWVMSYGERPYWDMTQDVINAEQDYRLPPP 848  
Db 798 PIRWTAPEAIQYRKFTSASDVNSYGIWVWVMSYGERPYWDMTQDVINAEQDYRLPPP 857  
Qy 849 MDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSGINPLDRT 908  
Db 858 MDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAWAPLSSGINPLDRT 917  
Qy 909 IPDYTSFNTVDWELEAIKMGQYKESFANAGFTSFVVVSQMMEDIILRLGVTLAGHQKIL 968  
Db 918 IPDYTSFNTVDWELEAIKMGQYKESFANAGFTSFVVVSQMMEDIILRLGVTLAGHQKIL 977  
Qy 969 NSIQVMRAQMNQIOSVEV 986  
Db 978 NSIQVMRAQMNQIOSVEV 995

## RESULT 6

US-10-029-020-60  
; Sequence 60, Application US/10029020  
; Publication No. US20040033971A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangolli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/10/029,020







Db 673 ERQRDFLSEASINGQFDHPNIRLEGVVKSRPVMILTFEMENCALDSFLRLNDGQFTV 732  
Qy 721 IOLVGLRGTAAGKYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTY 780  
Db 733 IOLVGLRGTAAGKYLSEMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTY 792  
Qy 781 TSALGGKIPTRWTAPEAIQVRKFTSASDVMSYGVVMEVMSYGERPYWDMNQDVINAIE 840  
Db 793 TSSUGGKIPTRWTAPEAIQVRKFTSASDVMSYGVVMEVMSYGERPYWDMNQDVINAIE 852  
Qy 841 QDYRLPPMDPCPSALHQLMDCWKQDRNHRPKFCQIVNTLDKMRNPSLKAMAPLSSGI 900  
Db 853 QDYRLPPMDPCPTALHQLMDCWDRNLRPKFSQIVNTLDKLRNAASLKVIASAQSGM 912  
Qy 901 NLPLDRTIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSOMMEDILRLGVTL 960  
Db 913 SQPLDRTVDPYTFVTGVDLDAIKMGYKESFVSAGFASFDLVAQMTAEDLLRIGVTL 972  
Qy 961 AGHOKKILNSTQVMRAQMNQIQSVEV 986  
Db 973 AGHOKKILNSTQVMRAQMNQIQSVEV 998

## RESULT 9

US-10-354-358-4  
; Sequence 4, Application US/10354358  
; Publication No. US20030157082A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc  
; APPLICANT: Hunter, John Joseph  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Tsai, Fong-ying  
; APPLICANT: Leeson, Andrea  
; APPLICANT: Lightcap, Eric S.  
; APPLICANT: Williamson, Mark  
; APPLICANT: Rudolph-Owen, Laura A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,  
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 5235,  
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,  
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,  
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,  
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,  
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES  
; FILE REFERENCE: MF102-020PIRNONIM  
; CURRENT APPLICATION NUMBER: US/10/354,358  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US 60/353,600  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 60/364,517  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/371,075  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: US 60/371,507  
; PRIOR FILING DATE: 2002-04-10  
; PRIOR APPLICATION NUMBER: US 60/372,984  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: US 60/374,194  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/382,995  
; PRIOR FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: US 60/385,023  
; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/388,853  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: US 60/389,395  
; PRIOR FILING DATE: 2002-06-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 998

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-354-358-4  
Query Match 70.6%; Score 3661.5; DB 14; Length 998;  
Best Local Similarity 70.2%; Pred. No. 8e-233;  
Matches 692; Conservative 116; Mismatches 159; Indels 19; Gaps 6;  
Qy 10 LLLPLLL-----AAVEETLMDSTTATAEGLGWVHPSPSGHEEYSGVDENNTTIRTYQCN 63  
Db 23 LLLPLLLPAGCALTEETLMDTKWTSELAMTSHPSGHEEYSGVDENNTTIRTYQCN 82  
Qy 64 VFESSQNNWLRTKFIERRGAHRTHVEMKFSVRCCSIPSPVSGCKETFNLYYYEADPDSA 123  
Db 83 VRESSQNNWLRTGFIWRDVORVYVELKFTVRDNCISIPNIPGCKETFNLFYEAUSDVA 142  
Qy 124 TKTFFNNMENPWVKVTIADADESFSQVDLGRVVKINTEVRSFGPVSRSGFYLAQDYG 183  
Db 143 SASSPFMENPYVKVDTIAPDESFSRLDAG---RVNTKVRSPGLSKAGFYLAQDGA 198  
Qy 184 CMSLIAVRVYRKCPIIQNGAIFQETLSGAESTSLVAARGSCIANAEVVDVPIKLYCNG 243  
Db 199 CMSLISVRAFYKCKASTTAGFALFPETLTGAETPSLVIAPGTCIPNAVEVSVPLKLYCNG 258  
Qy 244 DGEWLVPIGRCMCKAGFEAVENGTVCRGCPSGTFKANQGDCACTHCPINSRTTISEGATNC 303  
Db 259 DGEWVPVGNACTCATGHEPAKESQCRPCPGSYKAKQGEPCLPCCPNSRTTISPAASIC 318  
Qy 304 VCRNGYRADLDPDMPCTTIPSAQAVISSVNETSLMLEWTTPRDSGGREDLVYNIICK 363  
Db 319 TCHNFRADSDSADSACTTVPSPRGVISNVNETSLILEWSEPRDLGVARDLLYNNICK 378  
Qy 364 SC--GSGRGACTRCGNVOYAPROLGLTBRPIYISDLAHTQYTFEIQAVNGVTDOSPFS 421  
Db 379 KCHGAGGASACRCDNNEFVPRQLGSEPRVHTSHLAHRTVFEQAVNGVSGKSLP 438  
Qy 422 POPASVNITTNQAAPSAVSIHQVSRVDSITLSWSQDQPNQNGVILDYELQYKEKELSEY 481  
Db 439 PRVAANVITTNQAAPSEVPTLRHSSGSLTILSWAPPERNGVILLYEMKYFEK--SEG 496  
Qy 482 NATAKSPNTVTVQGLKAGAIYVQVARTVAGYRGYSGMYQFQWTE-AEYQTSIQEK 540  
Db 497 IASTVTQSMNSVOLQDLGRDARYVQVARTVAGYQYSRPABFETTSERGSQAQQLQEQ 556  
Qy 541 LPLIGSSAGLFLAVVIAIVCNRRGERADSEVTDKLOHYTSGHMTPGMKIYIDPF 600  
Db 557 LPLIVGSATAGLVFVAVVIAIVCNRRGERADSEVTDKLOHYTSGHMTPGMKIYIDPF 612  
Qy 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKREIFVAIKLXSGYT 660  
Db 613 TYEDPNEAVREFAKEIDVSCVKEEVIAGEFGEVCRGLKQPGREVFVAIKLXVGYT 672  
Qy 661 EKQRDFLSEASINGQFDHPNIRLEGVVKSRPVMILTFEMENCALDSFLRLNDGQFTV 720  
Db 673 ERQRDFLSEASINGQFDHPNIRLEGVVKSRPVMILTFEMENCALDSFLRLNDGQFTV 732  
Qy 721 IOLVGLRGTAAGKYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTY 780  
Db 733 IOLVGLRGTAAGKYLSEMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTY 792  
Qy 781 TSALGGKIPTRWTAPEAIQVRKFTSASDVMSYGVVMEVMSYGERPYWDMNQDVINAIE 840  
Db 793 TSSUGGKIPTRWTAPEAIQVRKFTSASDVMSYGVVMEVMSYGERPYWDMNQDVINAIE 852  
Qy 841 QDYRLPPMDPCPSALHQLMDCWKQDRNHRPKFCQIVNTLDKMRNPSLKAMAPLSSGI 900  
Db 853 QDYRLPPMDPCPTALHQLMDCWDRNLRPKFSQIVNTLDKLRNAASLKVIASAQSGM 912  
Qy 901 NLPLDRTIDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSOMMEDILRLGVTL 960  
Db 913 SQPLDRTVDPYTFVTGVDLDAIKMGYKESFVSAGFASFDLVAQMTAEDLLRIGVTL 972  
Qy 961 AGHOKKILNSTQVMRAQMNQIQSVEV 986





QY 304 VCRNGYRADLPDMPCTTIPSAQAVLSNVTSLMELWTPPRDSGGREDLVNIICK 363  
Db 328 TCHNFRYRADSASACTIVFSPRGVLSNNVTSLSLEWSEPRDLGVRODLLYVNIICK 387  
QY 364 SC--GSGRGACTCGDNVOYAPRQLGLTEPRIYISDILLAHTOYTEIOAVNGVTDOSPFS 421  
Db 388 KCHGAGGASACSRCDNVEFVRQLGLSEPRVHTSHLLAHTYTEFEVAVNGVSGKSPLP 447  
QY 422 POFASVNIITNOAAPSIVMHOVSRVTSDITLSWQDPQNGVILDELYEYKELSEY 481  
Db 448 PRYAANIITNOAAPSEVPTLHLHSSGSLTSLWAPPERNGVILDELYEYKELSEY 505  
QY 482 NATAIKSPNTVTVGLKAGAIYVQVRAVTVAGVGRYSGRMVFTWTE-AEYQTSQEK 540  
Db 506 IASTVTSQNSVQLDGLRPDARYVQVRAVTVAGVGRYSGRMVFTWTE-AEYQTSQEK 565  
QY 541 LPLITGSSAAGLVLIIVAVVIAVNCRRGFERADSEYTDKLQHTSGHMTGMIYIDPF 600  
Db 566 LPLIVGSATAGLVFVAVVIAVCLRKQRHGSSEYTEKLQY----IAPGMVYIDPF 621  
QY 601 TYEDDNEAVREPAKIDISCVKIEOVIGAGFGEVCSCHLKLPGKREIFVAIKLKSQYT 660  
Db 622 TYEDDNEAVREPAKIDISCVKIEOVIGAGFGEVCSCHLKLPGKREIFVAIKLKSQYT 681  
QY 661 EKQRDFLSEASIMQFDPHPNVHLEGVVTKSTPVMITFPMWNGSLDSFLRONDGOFTV 720  
Db 682 ERQRDFLSEASIMQFDPHPNIIRLEGVVTKSRPVMILTEPMWNCALDSFLRNDGOFTV 741  
QY 721 IOLVGLRGIAAGMKYLDAMVYVHRDLAARNILVNSNLVKVDSFGLSRFLEDDTSDPT 780  
Db 742 IOLVGLRGIAAGMKYLDAMVYVHRDLAARNILVNSNLVKVDSFGLSRFLEDDTSDPT 801  
QY 781 TSALGCKIPIRWTAPEALQYKFTSASDVWSYGVVMWMSYGERPYMDMTNODVNAIE 840  
Db 802 TSSLGCKIPIRWTAPEALQYKFTSASDVWSYGVVMWMSYGERPYMDMTNODVNAIE 861  
QY 841 QDYRLPPMDPCPSALHQLMLDCWQDRNHRPKFQIVNTLDKMRNPSNLKAMAPLSSGI 900  
Db 862 QDYRLPPMDPCPSALHQLMLDCWQDRNHRPKFQIVNTLDKMRNPSNLKAMAPLSSGI 921  
QY 901 NLPLDRTIPDYTSFNTVDEWLEAIKMOYKESFANAGFTSFVVSOMMEDILRLGVTL 960  
Db 922 SQPLDRTIPDYTSFNTVDEWLEAIKMOYKESFANAGFTSFVVSOMMEDILRLGVTL 981  
QY 961 AGHOKILNSIQVMRAQNMQIQSVEV 986  
Db 982 AGHOKILNSIQVMRAQNMQIQSVEV 1007

## RESULT 12

US-10-187-958-1  
; Sequence 1, Application US/10187958  
; Publication No. US20030170865A1  
; GENERAL INFORMATION:  
; APPLICANT: TAJIMA, HISAO  
; KITAGAWA, KOICHIRO  
; OHNO, HIROYUKI  
; UENO, TOSHIO  
; TITLE OF INVENTION: A No. US20030170865A1el Polypeptide of Protein p140  
; and DNAs encoding it  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10187,958  
FILING DATE: 03-Jul-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/558,340  
FILING DATE: 26-APR-2000  
APPLICATION NUMBER: 09/192,435  
FILING DATE: 08-JAN-1998  
APPLICATION NUMBER: 08/571,785  
FILING DATE: 13-DEC-1995  
APPLICATION NUMBER: 08/348,143  
FILING DATE: 23-NOV-1994  
APPLICATION NUMBER: JP 315806/1993  
FILING DATE: 24-NOV-1993  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 993 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: rat  
TISSUE TYPE: skeletal muscle myoblast  
CELL LINE: L6  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-187-958-1

Query Match 69.5%; Score 3603.5; DB 14; Length 993;  
Best Local Similarity 68.5%; Pred. No. 5.4e-229;  
Matches 680; Conservative 117; Mismatches 163; Indels 33; Gaps 6;  
QY 17 AAVEETLMDSTATA-----ELGMVHPSPSGWEVSGYDENMTIRTY 59  
Db 11 AAARAARAAATNSLSILVRPTSEGRIDSEFVELAWTSHPSGWEVSAIDSAMNPIRY 70  
QY 60 QVCNVFESSQNNWLRTKFIIRRGAIHIVEMKFSVRDCSSIPSPGCKETENLYVYAD 119  
Db 71 QVCNVRESSQNNWLRTGFIIRREVQVRYVELKFTVRDCNSIPNIPGCKETENLYVYAD 130  
QY 120 FDSATKTFPNWENPWKVDTTAADESQVDLGRVMKINTEVRSFGVPSGSGYLAFO 179  
Db 131 SDVASASSPFWMENPYKVDTTAPDESFSRLDAG---RVNTKVRSFGPLSKAGFYLAFO 186  
QY 180 DYGGCWSLIAVRFYRKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKL 239  
Db 187 DOGACMSLISVRAFYKCASTAGTALPPELTGAEPTSLVATPGTCLANAVEVSPVPLK 246  
QY 240 YCNGDEWLVPITGRCMKAGFEAVNGTVCRGCPSTFKANQGDACHTCPIINSRTTSEG 299  
Db 247 YCNGDEWLVPVVGACTCATGHEPAKETQCRACPPGSYKAKQGEPCPLCPNPSRTTSPA 306  
QY 300 ATNCVCRNGYRADLPDMPCTTIPSAQAVLSNVTSLMELWTPPRDSGGREDLVN 359  
Db 307 ASICTCHNFRADSDTADSACTTVPSPPRGVSNVNETSLILEWSEPRDLGGREDLVN 366  
QY 360 ITCKSCGSGRGA-----CTRCGDNVQYAPROLGLTEPRIYISDILLAHTOYTEIOAVNGV 414  
Db 367 VICKKCRGSSGAGGATCSRCDDNVEFVRQLGLSEPRVHTSHLLAHTYTEFEVAVNGV 426  
QY 415 TDOSPFSQFASVNIITNOAAPSIVMHOVSRVTSDITLSWQDPQNGVILDELYEY 474  
Db 427 SGKSLPPRYAAVNIITNOAAPSIVMHOVSRVTSDITLSWQDPQNGVILDELYEY 486  
QY 475 EKELSEYNATAIKSPNTVTVGLKAGAIYVQVRAVTVAGVGRYSGRMVFTWTE-AEY 533  
Db 487 EK--SKGIASVTSSQKNSVQLDGLRPDARYVQVRAVTVAGVGRYSGRMVFTWTE-AEY 544

534	QY	QT	SIOBKLPLIIIGSSAAGLVLIVVJAIVCNRRGFERADSEYTDKLOHYTSGHWTGCM	593
		:	:   :   :	
545	Db	AQOQLPILIVGSTVAGFVFWVVWVITALCLRKQRGPDAEYTEKLOQY----	VAPRM	600
		:	:   :   :	
594	QY	KIYIDPFTVEDNEAVRFAKEIDISCVKIEBOVIAGCFEGEVCSGHILKLPKREIFVAJK	653	
		:	:   :   :	
601	Db	KVIYDPTVEDNEAVRFAKEIDVSCVKIEVIGAGEFVEVCGRLLKLPORREVFAJK	660	
		:	:   :   :	
654	QY	TLKSGYTEQRDRDFISEASIMQGDHPNVIHLEGVTKSTPVMIIITEFMENGLSDFLRQ	713	
		:	:   :   :	
661	Db	TLKVGYTERQRDRDFISEASIMQGDHPNIIRLEGVTKSRPVMIITEFMENCALDSFLRL	720	
		:	:   :   :	
714	QY	NDGOFTVIOLVGMLRGIAGAEMKYLAADNNYVHRDLAARNILVNSNLCKVDGFSRFILED	773	
		:	:   :   :	
721	Db	NDGOFTVIOLVGMLRGIAGAEMKYISEMNYVHRDLAARNILVNSNLCKVDGFSRFILED	780	
		:	:   :   :	
774	QY	DTSDDPTYTSALGGKPIRWTAPEAIQYRKFTSASDVMSYGI VNMVMSYGERPYDMTNQ	833	
		:	:   :   :	
781	Db	DPSTDPTYTSLSGKPIRWTAPEAI DYRKFTSASDVMSYGI VNMVMSYGERPYDMNSNQ	840	
		:	:   :   :	
834	QY	DVINAEODRYLRPPMDCESALHQLMLDCWKDRNRHKPGCOIVNTLDKMRPNISKAM	893	
		:	:   :   :	
841	Db	DVINAVEQDYLRPPPMDCCPALHQLMLDCWVRDNRLRPKFSQIVNTLDKLI RNAASLKVI	900	
		:	:   :   :	
894	QY	APLSSGINPLLDRTIPDYTSFNTVDEMLEAIKMGOYKESFANAGFTSFDPVWSQMMEDI	953	
		:	:   :   :	
901	Db	ASAPSGMSQPLLDRTVPDYTTFTVTGVDMLDAIKMGRYKESFVGAGPASFDLVQAQMAEDL	960	
		:	:   :   :	
954	QY	LRLGVTLAGHQKIINSIQVMRAQNQIQSVTEV	986	
		:	:   :   :	
961	Db	LRIAGVTLAGHQKILSIQDMELQMNQOTLPQV	993	
		:	:   :   :	

## RESULT 13

```

US-10-408-765A-2942
; Sequence 2942, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC
; FILE REFERENCE: 660088 465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2942
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2942

```

	Query Match	69.3%	Score 3594.5	DB 16	Length 896
	Best Local Similarity	73.5%	Pred. No. 1.9e-228		
	Matches 655	Conservative 123	Mismatches 112	Indels 1	Gaps 1
Qy	90	MKESVRDCSSITPSVPGSKCTFNLYYYEADFSDATKTFPNWMEWPVKVDTIAADESFQ	149		
Db	1	MRFTVRDCSSLFNPVPGSKCTFNLYYYEADTSVIATKCSAFWSEAPYLLKVDITIAADESFQ	60		
Qy	150	VDLGGRVYMKINTEVRSFGPVSRSFGYLAFOYGGCWSLIAVRVYRCKPRIIQNGALFOE	209		
Db	61	VDFGRLMKYNTEVRSFGPLTNGFYLAFOYGCMSLLSVRFVFKKCPISVQNFVPE	120		
Qy	210	TLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRCMKCKAGFEAVENGTV	269		
Db	121	TMTCAESTSLVIARGCTPNAEEVDVPIKLYCNGDGEWMPVIGRCTCKPGYEP-ENSVA	179		

Qy	270	RGCPSGTFCANQGBEACHCPINSRSTTSEGATNCVCRNGYYPRADLDPLDMPCTTTPSPAQ	329
Db	180	KACPAAGTFCASQEAEGCSHCFSNRPASPAESPICTRCTGYTRADPDPPBEVACTSPVSGPR	239
Qy	330	AVISSVNETSLMLBWTTPRDSGGREDLVYNIICKSCSGRGACTCGDNQVQAPROLGLT	389
Db	240	NVISVNETSIILEWHPPRETGGRRDVTYNIICKCRADRSCSCRDDNVFVPRQLGLT	299
Qy	390	EPRIYISDLIAHTQYTEIOAQNNGVTDOSPSPQFASVNIITNQAAPSAVSIMHQVSRVY	449
Db	300	ECRVISISLWAHTYFTEDIOAINGVSSKPPFPQHVSVNIITNQAAPSTVPIMHQVSATM	359
Qy	450	DSITLSSQPDPONGVILDYELQYVEKELSSYNATAIKSPNTVTVQGLKACAIYVQVQR	509
Db	360	RSITLSPQEPQNGIILDYEIRYIEKEHNFSNMSARSTNTARIDGLRPGWYVYVQVR	419
Qy	510	ARTVAGYGRYSGKMYFQMTBAEYQTSIOEKLPLIIGSSAAGLVFLIAVVJIAVCNRRG	569
Db	420	ARTVAGYCKFSKGMCFQTLTDDDYKSELREQULIAGSAAAGVFWFVSAIVSAISVCRRK	479
Qy	570	PERADSEYTKLQHYTSGHMTPGMKIYIDPTFYEDPNEAVREFAKEIDISCVKIEOVIGA	629
Db	480	AYSKEAVYSDKLQHYSTGRGSPGMKIYIDPTFYEDPNEAVREFAKIDVSVFKIEEVIGA	539
Qy	630	GEFGEVCSGHLKLPKGREIYFVAIKTLKSGYTEKQRRDFLSEASIMGQDPHPNVIHLEGVY	689
Db	540	GEFGEVYKGRLLKPKGREIYVAIKTLKAGYSEKQRRDFLSEASIMGQDPHPNIIIRLEGVY	599
Qy	690	TKSTPVMIIITFPMENGSLDSEFLRQNDGQFTYIOLVGLMRLGTAAGMKYLADMYVHRDLAA	749
Db	600	TKSRPVMIIITFPMENGALDSEFLRQNDGQFTYIOLVGLMRLGTAAGMKYLAEMYVHRDLAA	659
Qy	750	RNILLVNSNLCKVSDFGLSRLEDDTSDPTTYSALGGKIPIRWTAPAEIAYRKFTSASDV	809
Db	660	RNILLVNSNLCKVSDFGLSRYLQDDTSDPTTYSLLGGKIPVRWTAPAEIAYRKFTSASDV	719
Qy	810	WSYGIYVWVWMSYGERPYWDMNQDVINAIEQDYVPLPPMDCPSEALHQLMLCQWKDRNH	869
Db	720	WSYGIYVWVWMSYGERPYWDMNSQDVINAIEQDYVPLPPMDCPSEALHQLMLCQWKDRNS	779
Qy	870	RPKFGQIVNTLDKMIIRNPNSLUKAMAPLSSGNLPLLDRTIPDYTSFNTVDEMLEAIKMGQ	929
Db	780	RPRFAEIVNTLDKMIIRNPASPALKUTVATITVAFVSQPLLDRSIDPDTAFITVDDMLSAIKMVQ	839
Qy	930	YKESFANAGFTSFDFVVSOMMEDILRGLVTLAGHQKILNLSIQVMRAQMNQ	980
Db	840	YRDSFLTAGFTSLOLVMTQTSIEDLLRIGITLAGHQKILNLSIHSVRVOISQ	890

RESULT 14

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```



```
Db 141 ---NIKENQYIKIDTIAADESFTDLGDRVMKLNTEVRDVGPLSKGKGFYLAFOVGACI 197
Qy 186 SLIAVRVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEEDVDPIKLYCNGDG 245
Db 198 ALVSRVYRKCPSPVHLAVFPDTITIGADSSQLLEVSGSCV-NHSTDEPPKMHCSAEG 256
Qy 246 EWLPIGRCKMCKAGFEAVENGTVCRGCPSTGTFKANQDEACTHCPINSRTTSEGATNCVC 305
Db 257 EWLPIGRCKMCKAGYEE-KNGT-CQVCRPGFFKASPHIQSCGKCPHSHYTHEEASTSCVC 314
Qy 306 RNGHYRADLDPLDMPCTTIISAPQAVISSNETSLMLEWTPPRDSCGREDLVNIIKSC 365
Db 315 EKDYFRRESPPPTWACTRPPSAPRNAISNVNETSVFLEWIPADTGRKDVSVYIACKKC 374
Qy 366 GSGRGACTRCGDNVQVAPQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFA 425
Db 375 NSHAGVCECGHVRVYLPQSGGLKNTVMVVDLHAHTYTFEIOAVNGVTDQSPSPQFA 434
Qy 426 SVNITTNQAAPSAYSIMHQSRTVDSITLSNSQDPNGVILDYELQYKEKELSEYNATA 485
Db 435 SVNITTNQAAPSPVTVKKGKIAKNSISLSQWEDPENGILLEYEIKHFEKD-QETSYTI 493
Qy 486 IKSTPTNTVOGLKAGAIYFQVQARTVAGRGYSGKMYFQTMTEASYQTSIQEKLPIII 545
Db 494 IKSKETTITAEGLKPAVYFQIRARTAAGYGFVSRFEPET-TPVPAASSDQSQIPIVIA 552
Qy 546 GSSAAGVFLJAVVVAIVCNRRGFERADSEYTDKLOHYTSGHM-TPGMKIYIDPFTYED 604
Db 553 VSVTVGVILLAVVIGVLLSGRCYSAKQDPEEEKWHFHNGHILKPGVRTYIDPHTYED 612
Qy 605 PNEAVRFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKGRKELFVAIKLKGSTTEKOR 664
Db 613 PNQAVHEFAKEIEASCITIERVIGAGEFGEVCSGRLKLPKGRKELPVAIKLVGYTEKOR 672
Qy 665 RDLSEASIMQFDPHPNVHLEGVYTKSTPMIITEFWENGSLDSFLRQNDGQFTVQLV 724
Db 673 RDLSEASIMQFDPHPNIIHLEGVYTKSPVMIVTEYMWENGSLDTFLKQNDGQFTVQLV 732
Qy 725 GMLRGIAAGMKYLDAMNVVHRDLAARNILVNSNLVCKVSPGLSRFLEDDTSDPTYSAL 784
Db 733 GMLRGISAGMKYLDGMYVHRDLAARNILVNSNLVCKVSPGLSRVLEDD-PEAYTTR- 790
Qy 785 GKKIPIRWTAPEAIQYRKFTSASDVWSYGIWMVEVMSYGERPYWDMTNQDVINAIEQDYR 844
Db 791 GKKIPIRWTAPEAIAFRKFTSASDVWSYGIWMVEVMSYGERPYWDMTNQDVIKAVEGYR 850
Qy 845 LPPMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMKINPNSLKAMAPLSSGINLPL 904
Db 851 LPSMDCPSAALYQLMDCWQKERNRPKFDIENVMLDKLIRNPSLKLTVNASCRVSNLL 910
Qy 905 LDRTPDYTSFNTVDEWLEALIKMGQYKESPANAGFTSFVVSOMMEDILRLGVTLAGHQ 964
Db 911 AEHSPLASGATRGVGEWLEALIKMGYTEIFMWENGTSMDAVAQVTLSDRLRLGVTLAGHQ 970
Qy 965 KKIILNSIQVMRAQM 978
Db 971 KKIILNSIQVMKVQL 984
```

## RESULT 16

```
US-10-412-277-7
; Sequence 7, Application US/10412277
; Publication No. US20030175791A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001067DIV
; CURRENT APPLICATION NUMBER: US/10/412,277
; CURRENT FILING DATE: 2003-04-14
; NUMBER OF SEQ ID NOS: 8
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 7
```

```
; LENGTH: 953
```

```
; TYPE: PRT
```

```
; ORGANISM: Human
```

```
; US-10-412-277-7
```

## Query Match

```
Best Local Similarity 58.8%; Score 3048; DB 14; Length 953;
```

```
Best Local Similarity 59.2%; Pred. No. 2,4e-192;
```

```
Matches 568; Conservative 164; Mismatches 216; Indels 12; Gaps 9;
```

```
Qy 20 EETLMDSITTATAEGLGMVHPSPSWEBEVSVDENMNTIRTYQVNCVPESSONMLRTFPIR 79
Db 3 EVNLLDSRTVMGLDGIATFAPKNGWIEGIDENYAPIHTYQVCKWBEQONNNLLTSWIS 62
Qy 80 RRGARHIVHMKFSVRDCSSIPSPGSKETENLYXYEADFDSATKTFPNNMENPMVKVD 139
Db 63 NEGASRIPIELKATFLRDCNSLPGLGTCKETFNMYFESDDQNGR----NIKENQYIKID 118
Qy 140 TIAADESFQSDVILGGRVMKINTEVRSGFVSRSGFVLAFOYDYGCMSLIAVRVYRKCPR 199
Db 119 TIAADESFTELDLDGRVMKLNTEVRDVGPLSKGKGFYLAFOVGACIALVSRVYKCPKS 178
Qy 200 IIONGAIFQETLSGAESTSLVAARGSCIANAEEDVDPIKLYCNGDGEWLPIGRCKMCKAG 259
Db 179 VVRHLAVFPDTITIGADSSQLLEVSGSCV-NHSTDEPPKMHCSAEGEWLPIGRCKMCKAG 237
Qy 260 FEAVENGTVCRGCPSTGTFKANQDEACTHCPINSRTTSEGATNCVCNRYRDLPLDM 319
Db 238 YEE-KNGT-CQVCRPGFFKASPHIQSCGKCPHSHYTHEEASTSCVCEKDYFRRESDPPTM 295
Qy 320 PCTTIPSAPQAVISSNETSLMLEWTPPRDSCGREDLVNIIICKSCGSGACTRCGDNV 379
Db 296 ACTRPPSAPRNAISNVNETSVFLEWIPADTGRKDVSVYIACKKCNHAGVCECGHV 355
Qy 380 QYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNTTNQAASAV 439
Db 356 RYLPQSGGLKNTVMVVDLHAHTYTFEIOAVNGVTDQSPSPQFASVNTTNQAASAV 415
Qy 440 SIMHQSRTVDSITLSNSQDPNGVILDYELQYKEKELSEYNATAIKSPNTNTVVOGLK 499
Db 416 TNVKGKIAKNSISLSQWEDPENGILLEYEIKHFEKD-QETSYTIKSKETTITAEGLK 474
Qy 500 AGAIYFQVQARTVAGRGYSGKMYFQTMTEASYQTSIQEKLPIIIGSSAAGLVFLIAY 559
Db 475 PASVYVFIQARTAAAGYGFVSRFEPET-TPVPAASSDQSQIPIVIAVSVTVGVILLAVI 533
Qy 560 VIAIVCNRRGFERADSEYTDKLOHYTSGHM-TPGMKIYIDPFTYEDNEAVRFAKEIDI 618
Db 534 GVLLSGRCYSAKQDPEEEKWHFHNGHILKPGVRTYIDPHTYEDPNQAVHEFAKEIEA 593
Qy 619 SCVKIEQVIGAGEFGEVCSGHLKLPKGRKELFVAIKLKGSTTEKORRDLSEASIMQFD 678
Db 594 SCITIERVIGAGEFGEVCSGRLKLPKGRKELPVAIKLVGYTEKORRDLSEASIMQFD 653
Qy 679 HPNVHLEGVYTKSTPMIITEFWENGSLDSFLRQNDGQFTVQLVGMRLGIAAGMKYLA 738
Db 654 HPNIIHLEGVYTKSPVMIVTEYMWENGSLDTFLKQNDGQFTVQLVGMRLGIAAGMKYLS 713
Qy 739 DMNVVHRDLAARNILVNSNLVCKVSPGLSRFLEDDTSDPTYSALCGKPIRWTAPAI 798
Db 714 DMGVHRDLAARNILVNSNLVCKVSPGLSRVLEDD-PEAYTTR-GKKIPIRWTAPEAI 771
Qy 799 QYRKFTSASDVWSYGIWMVEVMSYGERPYWDMTNQDVINAIEQDYRILPMDPCPSALHQL 858
Db 772 AFRKFTSASDVWSYGIWMVEVMSYGERPYWDMTNQDVIKAVEGYRLPSPMDCPAALYQL 831
Qy 859 MLDWCQKDRNHRPKFGQIVNTLDMKINPNSLKAMAPLSSGINLPLDRTIPDYTSFNTV 918
Db 832 MLDWCQKERNRPKFDIENVMLDKLIRNPSLKLTVNASCRVSNLLAEHSPLASGATRGV 891
Qy 919 DEWLEALIKMGQYKESPANAGFTSFVVSOMMEDILRLGVTLAGHQKILNSIQVMRAQM 978
Db 911 DEWLEALIKMGQYKESPANAGFTSFVVSOMMEDILRLGVTLAGHQKILNSIQVMRAQM 978
```

Db 892 GEWLEAIKMGRTYEIFWENGYSMDAVAQVTLLEDRLLGLVTLVGHCKIMNSLOEKVQL 951

RESULT 17  
US-10-723-860-597  
; Sequence 597, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 597  
; LENGTH: 986  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-723-860-597

Query Match 58.7%; Score 3045; DB 17; Length 986;  
Best Local Similarity 59.3%; Pred No. 3.9e-192; Indels 40; Gaps 12;  
Matches 580; Conservative 146; Mismatches 212

QY 18 AVEETLMDSTATABELGMVHP-PGMEVEVSGYDENMNTIRTYQCVNPFSSQNNWLRTK 76  
Db 28 ANEVTLLDSRSVQGLGWIASPLEGGEVSEIMDEKNTPIRTYQCVNMFPSQNNWLRTD 87  
QY 77 FTRREGARHIVHEKFSVDCSSIPSPVSCKEFNLYHYEADTSDATKTFPNMENPWV 136  
Db 88 WITREGARVIEIKFTLLDNCNLPVGMGTCKETFNLYYESDNDKERFI-----RENQFV 143  
QY 137 KVDITADESPQVDLGRVNMKINTEVRSGFVRSRSGFYLAQDYGCMSLIAVRVYRK 196  
Db 144 KIDITADESTQVDIGDRIMKLNTEIRDVGLSKGFLYLAQDVGACIALSVRVYRK 203  
QY 197 CPRIIONGAIQFETLSGABSTSLVAARGSCSIANAEEVDVPIKLYCNGDGEWLVPICRMC 256  
Db 204 CFLTARNLAQPDPTITGADTSSLVVRGSCVNNSEKDVV-KMYCGADGEWLVPICNLC 262  
QY 257 KAGFEAVENGTVCRGCPSTGTFKANOGBEACTHCPIINSRTTSEGATNCVCRNGYVRADLDP 316  
Db 263 NAGHE--ERSGECQACKIGYKALSTDTACKCPHSHVWEGATSCCTDRGFPRADNDA 320  
QY 317 LDMPTTIPSAQVIVSNETSMLLEWTPPRDSGGREDLVNIIICKSCGSG-RGACTRC 375  
Db 321 ASMECTRPSPAPLNLISNVNETSVNLEWSSPQNTGGRQDISYNVCKKCGAGDPKCRPC 380  
QY 376 GDNVOYAPROGLTEPRIYISDLIAHTQYTFEQAQVNGVTDQSPFPQFASVNTITNOAA 435  
Db 381 GSGVHYTPQOGLTKTKVSTDLIAHTNYTFEIAVNGVSKYNNPNDQSVSVTVTTNOAA 440  
QY 436 PSAYSIMHOVSRTVDSITLSWSQDQPNQVILDYELQYVEKSELSEYNATAIKSPPTNTTV 495  
Db 441 PSSIALVQAEVTRYVALAWLEDRPNVILEVYKYEKQDNERSYRIVRTAARTDI 500  
QY 496 QGLKAGAIYFOVARTVAGRYSGKMYFQTMTEABYQTSIOEKLPL-LIIGS-----547  
Db 501 KGLNPLTSYFHFARTAAGYGFSEPLEVTNT-----VPSRIIGDGANSTVL 549  
QY 548 --SAAGLVFLIAVVIIVCNRR--GPERADSEYTKLQHTYSGHMTPGMKIYIDPFTYE 603  
Db 550 LVSVSGSVLWLVILIAFVLSRRSKYSKAKQADEE-----KHLNQGVRTYVDPFTYE 603  
QY 604 DPNEAVREFAKEDIDSCVKEQVIGAGEFCGSCGHLKPLGKREIFVAIKTLKSGYTEKQ 663  
Db 604 DPNQAVREFAKEIDASCIEKIVGIGVGEFCGSCGHLKPLGKREICVAIKTLKAGYTDKQ 663

664 RRDFLSEASIMGQFDHPNVIHLEGVVTKSTPVMIIIFEMENGSLDSFLRQNDGQFTVQL 723  
Db 664 RRDFLSEASIMGQFDHPNVIHLEGVVTKSTPVMIIIFEMENGSLDAFLRQNDGQFTVQL 723  
QY 724 VMLRGIAAGKYLADNMYVHRDLAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTVISA 783  
Db 724 VMLRGIGSGMKYLSDMYSYVHRDLAARNILVNSNLVCKVSDFGMSKRVLEDD-PEAAVTR 782  
QY 784 LGGKIPIRWTAPRAIOYRKETSASDVMSYGVIMVMEVMSYGERPYWDMTQDVINAIEODY 843  
Db 783 -GGKIPIRWTAPRAIAYRKETSASDVMSYGVIMVMEVMSYGERPYWDMTQDVILKAEEGY 841  
QY 844 RLPPMDPCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLP 903  
Db 842 RLPPMDPCIALHQLMLDCWQKERSDRPKFGQIVNMVLDKLRNPNSLKRTGTESSRPNTA 901  
QY 904 LLDRTTIPDYTSFNTVDLEWLEAIKMGQYKESFANAGTSTFSDVVSQMMEDILRLGVTLGH 963  
Db 902 LLDPSPEFSASVSVGMDLQAIKMDRYKDNFTAAAGYTTLEAVVHVNQEDLARIGITATH 961  
QY 964 QKKILANSIQWRAQMNQI 981  
Db 962 QNKILSSVQAMRTQMQM 979

RESULT 18  
US-09-823-187-39  
; Sequence 39, Application US/09823187  
; Publication No. US20030096952A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Padigaru, Muralidhar  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Taupier, Raymond J  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-745  
; CURRENT APPLICATION NUMBER: US/09/823,187  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/193,339  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/193,205  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/195,343  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: 60/195,088  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,005  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,792  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: 60/196,556  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: 60/197,081  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/197,525  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/197,087  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 993  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-823-187-39

Query Match		58.6%; Score 3038.5; DB 10; Length 993;
Best Local Similarity		59.3%; Pred. No. 1.1e-191;
Matches		573; Conservative 153; Mismatches 225; Indels 15; Gaps 8;
Qy	17	AAVEETLMDSTTATAGLWVHPSPGSEVSGYDENMTTIRTYQVNCVFPSSQNNWLRTK 76
Db	29	AAKEVILLDSKAQOTELEWISSPPNGWEEISGLDENYTPRTYQVQCVMESQNNWLRTN 88
Qy	77	FIRRGAGHRHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFSATKTFPNMNPV 136
Db	89	WIAKSNQRIFFVELKXETLRLDCNSLPGLGCKETFNLYYETDYD----TGRNIRENQYV 144
Qy	137	KVDTIAADESFSQVLDGGRVMKINTEVRSPGVSFGYLAFOYGGCMLSIAVRVYRK 196
Db	145	KIDTIAADESFTQDLGERKMKLNTREVRIGPLSKGFGYLAFOYGGCMLSIAVRVYRK 204
Qy	197	CPRIIONGATFOETLSGAESTSLVAARGSCIANA-BEVDVPIKLYCNGDGEWLVPIGRM 255
Db	205	CWSIIENLAIPDPTVTGSEFSSSLVEVRGTCVSSABEEAENSPKMHCSABGEWLVPIGKCI 264
Qy	256	CKAGFEAVENGTVCRGCPSTFKANQDGEACTHCPINSRTTSEGATNCVCRNGYRADLD 315
Db	265	CKAGYQ--QKGDTCPCGRGFYKSSQDLQCSRCPHSPDSEKSSRCDSDSYRAPSD 322
Qy	316	PLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGREDLVNITCKSCSGRGACTRC 375
Db	323	PPYVACTRPPSAPQNLFINQTTVLSWSPADNGRNDVTYRLCKRCSWEQGEVCP 382
Qy	376	GDVQVAPROLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFQFASVNTTNOAA 435
Db	383	GSNIGYMPQQTGLVDNVTVMDDLHANYTFEVEAVNGVSDLSRQSLFAAVSITTGQAA 442
Qy	436	PSAVSIMHOVSRTVDSITLSQSDQPNGLVDYELQYKELSEYNATAIKSPNTNVTV 495
Db	443	PSQVSGVWKERVLSQSEVHPNGVITEIKIYENDQREYRSTVTKSTGASI 502
Qy	496	QGLKAGAIYVQVARTVAGRYSGKQYFQMTAEABYQTSIQEKLPLIIGS--SAAGLV 553
Db	503	NNLKPGTVVYQIRAFATAGYGNYSRPLDVLATLEATATAVSSBONPVIIIAVVAVAGTI 562
Qy	554	FLIAVVAIVCNRR-GFERADSEYTKLQHYSGHMTGPKMIYIDPFTYEDNEAVREF 612
Db	563	ILVPMVFGFIIRRHGYSKADQGBELVPH---FKPPGKTYYIDPFTYEDNEAVRHQF 619
Qy	613	AKEDISCVKEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDLSEAS 672
Db	620	AKELDASCIIKERVIGAGEFGEVCSGRKLPGRKRDVAIKLVKGYTERKQRDLCEAS 679
Qy	673	IMGQFDHPNVHLEGVVTKSTPVMIIITPEMNGSLDSFLRQNDGQFTVIQLVGMRLGIAA 732
Db	680	IMGQFDHPNVHLEGVVTRGKPMVIEYMEAGALDAFLKHDQFTVIQLVGMRLGIAA 739
Qy	733	GMYLADNMVYHRLAARNILVNSNLVKVSDFGLSRFLDDTSDPTTYSALGKPIRW 792
Db	740	GMYLADNMVYHRLAARNILVNSNLVKVSDFGLSRFLDDTSDPTTYSALGKPIRW 797
Qy	793	TAPAIQVRFKTSASDVWSYGVIMVWYSGERYPDMWNTQDVINATEQDYRLPPMDCP 852
Db	798	TAPAIQVRFKTSASDVWSYGVIMVWYSGERYPDMWNTQDVINATEQDYRLPPMDCP 857
Qy	853	SALHQLMDCQKQDRNHRPFGQIVNTLDKMRNPNLSKAMAPLSSGINFLPLDRTIPDY 912
Db	858	AGLHQLMDCQKQGERGRPFQIVGLIDKMRNPNLSKTPGLGCSRPIPLDQNTPDF 917
Qy	913	TSFNTVDEWLEAIKQGOYKESFANAGTSPDVUSQMMEDILRLGVTLAGHOKILNSIQ 972
Db	918	TTFCVSGEWLQAIKQERYKONFTAAAGYNLSLESVARTMIEDVMSLIGITLVGHQKIMSSIQ 977
Qy	973	VMRAQM 978
Db	978	TMRAQM 983

RESULT 19  
US-09-823-187-41  
; Sequence 41, Application US/09823187  
; Publication No. US20030096952A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgees, Catherine  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Padigar, Muralidhar  
; APPLICANT: Patturajan, Meera A  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Taupier, Raymond J  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-745  
; CURRENT APPLICATION NUMBER: US/09/823,187  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/193,339  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/193,205  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/195,343  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: 60/195,088  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,005  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,792  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: 60/196,556  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: 60/197,081  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/197,525  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/197,087  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 41.  
; LENGTH: 993  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-823-187-41

Query Match 58.6%; Score 3038.5; DB 10; Length 993;  
Best Local Similarity 59.3%; Pred. No. 1.1e-191;  
Matches 573; Conservative 153; Mismatches 225; Indels 15; Gaps 8;  
Qy 17 AAVEETLMDSTTATAGLWVHPSPGSEVSGYDENMTTIRTYQVNCVFPSSQNNWLRTK 76  
Db 29 AAKEVILLDSKAQOTELEWISSPPNGWEEISGLDENYTPRTYQVQCVMESQNNWLRTN 88  
Qy 77 FIRRGAGHRHIVEMKFSVRDCSSIPSPGSKETFNLYYEADFSATKTFPNMNPV 136  
Db 89 WIAKSNQRIFFVELKXETLRLDCNSLPGLGCKETFNLYYETDYD----TGRNIRENQYV 144  
Qy 137 KVDTIAADESFSQVLDGGRVMKINTEVRSPGVSFGYLAFOYGGCMLSIAVRVYRK 196  
Db 145 KIDTIAADESFTQDLGERKMKLNTREVRIGPLSKGFGYLAFOYGGCMLSIAVRVYRK 204  
Qy 197 CPRIIONGATFOETLSGAESTSLVAARGSCIANA-BEVDVPIKLYCNGDGEWLVPIGRM 255  
Db 205 CWSIIENLAIPDPTVTGSEFSSSLVEVRGTCVSSABEEAENSPKMHCSABGEWLVPIGKCI 264  
Qy 256 CKAGFEAVENGTVCRGCPSTFKANQDGEACTHCPINSRTTSEGATNCVCRNGYRADLD 315  
Db 265 CKAGYQ--QKGDTCPCGRGFYKSSQDLQCSRCPHSPDSEKSSRCDSDSYRAPSD 322  
Qy 316 PLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGREDLVNITCKSCSGRGACTRC 375

Db 323 PPVACTRPPSPONLIENINQTTVSLEWSPADNGRNDVTYRLCKRCSWEQECVPC 382  
Qy 376 GDNVQAPRQLGTEPRYIYISDLAHTQYTFIQAQVNGVTDOSPSPOPASVNIITNOAA 435  
Db 383 GSNIGYMPQOTGLVDNVYVMDLLAHANTFEVAVNGVSDLSRSLRFAAVSITGQAA 442  
Qy 436 PSAVSIHMQVSRVDSITLSWQOPDOPNGVILDYLOYYEKELSEYNATAIKSPINTVTV 495  
Db 443 PSQVSGVMKERVLSRVELSWQEPHNGVITFEIKYKQORERTYSTVKTSISASI 502  
Qy 496 QGLKAGAIYVQVARTVAGYGRYSGMYFQMTAEYQTSIQEKLPLIIGS--SAAGLV 553  
Db 503 NNLKPGTVVFOIRAFPTAGYGNYSRPLDVATLEATATAVSSEQNVIIIAVAVAGTI 562  
Qy 554 FLIAVVVIAVCNRR--GPERADSEYTDKLOHTSHTMTPGMKIYIDPTEYEDPNEAVREP 612  
Db 563 ILVFWFGIIGRRHCGYSKADQEGDEELYPH---FKFFGKTYIDPTEYEDPNRAVHQF 619  
Qy 613 AXEIDISCVKIRQVIGAGFGEVCSGHLKLPGRKIFVAIKTLKSGYTEKORRDPFLSEAS 672  
Db 620 AKELDASCIIKERVIGAGFGEVCSGRLKLPGRKDVAVAIKTLKGYTEKORRDFLCEAS 679  
Qy 673 INGOFDHNVHLEGVTKSTPWTMITFPMENGLSDSFLRQNDGQFTVIQVGMRLGIAA 732  
Db 680 INGOFDHNVHLEGVTKSTPWTMITFPMENGLSDSFLRQNDGQFTVIQVGMRLGIAA 739  
Qy 733 GMKYLADMYVHRDLAARNILVNSNLCKVSDFGLSRLEDDTSDPTVTSALGGKIPRW 792  
Db 740 GMYLADMGVHRDLAARNILVNSNLCKVSDFGLSRLEDDTSDPTVTSALGGKIPRW 797  
Qy 793 TAPEAIQYRKFTASDVMSYGIWMEVMSYGERPYWDMTNDQVINAIEQDYRLPPMDCP 852  
Db 798 TAPEAIQYRKFTASDVMSYGIWMEVMSYGERPYWDMTNDQVINAIEQDYRLPPMDCP 857  
Qy 853 SALHQLMDLCKQKRNHRPKGOIVNTLDKMRPNLSKAWAPLSSGILNPLDRTIPDY 912  
Db 858 AGHLQMLDCKQKGERPKPEQIVGILDKMRPNLSKPLGTCRSPISPLDQNTPDF 917  
Qy 913 TSFNTVDEWLEAIKMGQYKESFANAGFTSPDVWSQMMEDILRLGVLTAHGHOKILNSIQ 972  
Db 918 TTFCSVGEWLQAIKMYKDNFTAGYNSLESVARMTIEDVMSLGIILVGHQKIMSIO 977  
Qy 973 VNRQOM 978  
Db 978 TMRQOM 983

## RESULT 20

US-09-982-610-36  
; Sequence 36, Application US/09982610  
; Patent No. US20020146420A1

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
Bennett, Brian D.  
Goeddel, David  
Lee, James M.  
Matthews, William  
Tsai, Siao Ping  
Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/982.610

FILING DATE: 17-Oct-2001

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/446,648

FILING DATE: 1996-MAY-23

APPLICATION NUMBER: 08/222616

FILING DATE: 04-APR-1994

## ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0821P3PCT

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

## INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 1104 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-982-610-36

Query Match 58.6%; Score 3038; DB 9; Length 1104;

Best Local Similarity 59.3%; Pred. No. 1.3e-191;

Matches 580; Conservative 145; Mismatches 213; Indels 40; Gaps 12;

Qy 18 AVETILMDSITATAELGMMVHP-PSGWEVSGVDENMTIRTYQVCNVPESSONWLRTK 76

Db 28 ANEVTLDSRVSQELGWTASPLEGWEVSIWDEKNTPIRTYQVCNVPESSONWLRTD 87

Qy 77 FIRRGARHIVHKFSVRDCSSIPSVPSCSKETFNLYYYEADFDSATKTFPNWMPV 136

Db 88 WITREGAQRVYIETKFLRDCNSLPGVMGTCKETNLYYESDNDKERFI---RENQV 143

Qy 137 KVDITAAADSFQVLDGGRVMKINTEVRSFGVSRSGFVLAFOYGGCNSLIATVAVFYRK 196

Db 144 KIDTIAADSFQVLDGGRVMKINTEVRSFGVSRSGFVLAFOYGGCNSLIATVAVFYRK 203

Qy 197 CPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRWC 256

Db 204 CPLTVNLAAQFPDTITGADTSSLVEVRGSCVNNSEKQVP-RMYCGADGEWLVPIGNCLC 262

Qy 257 KAGFAVENGTVCRCPSGTFFKANQDEACTHCPINSRTTSEGATNCVCRNGYYRADLDP 316

Db 263 NAGHE--ERSGCOACKIGYIKALSTDATCAKCPHYSVWEGATSCCTCDRGFFRADNDA 320

Qy 317 LDMPTCTTPSAPQAVISSVNETSLMLEWTPPRDSSGREDLVNIIICKSGSG-RGACTRC 375

Db 321 ASMPCTRPPSAPLNLISNVNETSVNLEWSSPONTGRODISYNNVCKKCGAGDPKCRPC 380

Qy 376 GDNVQAPRQLGTEPRYIYISDLAHTQYTFIQAQVNGVTDOSPSPOPASVNIITNOAA 435

Db 381 GSGVHYTPQONGKLTGKSITDLLAHTNYTEIWAIVNGVSKYNPNPDQSVSVTVTTNOAA 440

Qy 436 PSAVSIHMQVSRVDSITLSWQOPDOPNGVILDYLOYYEKELSEYNATAIKSPINTVTV 495

Db 441 PSIALVQAKVETRYSVLAWLEPDRPNGVILEYKYEKQDNERSYRIVTAARNTDI 500

Qy 496 QGLKAGAIYVQVARTVAGYGRYSGMYFQMTAEYQTSIQEKLPL-LIIGS----- 547

Db 501 KGLNPLTSYVPHVARTAAAGYDGFSEPLEVTNT-----VPSRIIGDGANSTVL 549

Qy 548 --SAGLVFLIAVVVIAVCNRR--GPERADSEYTDKLOHTSHTMTPGMKIYIDPTEY 603

Db 550 LVSVSGSVVVLVILIAAFVIRRRSKYSKAKQAEDE-----KELNQGVRTYDPTEY 603

Qy 604 DPNEAVREFAKEIDISCVKIEQVIGAGFGEVCSGHLKLPGRKIFVAIKTLKSGYTEKQ 663

Db 604 DPNOAVREFAKEIDASCIIKIEKVIGFGEVCSGRLKVPGRKREICVAIKTLKAGYTDKQ 663



Qy 664 RRDFLSASIMQGFDPHNVHLEGVVTKSTPVMITFEMENGSLDSFLRQNDGQFTVIQL 723  
Db 664 RRDFLSASIMQGFDPHNVHLEGVVTKSTPVMITFEMENGSLDSFLRQNDGQFTVIQL 723  
Qy 724 VGLMGLTAAAGKYLADNNYVHRDLAARNILVNSLVCKVSDPGLSRFLEDDTDPYTTSA 783  
Db 724 VGLMGLTAAAGKYLADNNYVHRDLAARNILVNSLVCKVSDPGLSRFLEDDTDPYTTSA 783  
Qy 784 LGGKIPIRWTAPEAIQYRKFTSASDVMSYGIVMVEVMSYGERPYWDMNQDINAIQDDY 843  
Db 784 LGGKIPIRWTAPEAIQYRKFTSASDVMSYGIVMVEVMSYGERPYWDMNQDINAIQDDY 843  
Qy 844 RLPPMDCPSALHQLMDCQKORNRHPRKFGQIVNTLDMKMRNPNLSKAMAPLSSGNLP 903  
Db 844 RLPPMDCPSALHQLMDCQKORNRHPRKFGQIVNTLDMKMRNPNLSKAMAPLSSGNLP 903  
Qy 904 LLDRTIPDYSFNTVDEWLEAKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGH 963  
Db 904 LLDRTIPDYSFNTVDEWLEAKMGQYKESFANAGFTSPDVVSQMMEDILRLGVTLAGH 963  
Qy 964 QKILNLSQVMAQWQNI 981  
Db 964 QKILNLSQVMAQWQNI 981  
Qy 962 QNKILSSQVMAQWQNI 979  
Db 962 QNKILSSQVMAQWQNI 979

RESULT 21  
US-10-316-124-3  
; Sequence 3, Application US/10316124  
; Publication No. US20030152574A1  
; GENERAL INFORMATION:  
; APPLICANT: Logan, Thomas Joseph  
; APPLICANT: Chun, Miyoung  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210  
; FILE REFERENCE: MP101-291P1EM  
; CURRENT APPLICATION NUMBER: US/10/316,124  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR FILING DATE: 2002-12-10  
; PRIOR FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1037  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-316-124-3

Query Match 58.5%; Score 3036; DB 14; Length 1037;  
Best Local Similarity 57.6%; Pred. No. 1.6e-191;  
Matches 574; Conservative 165; Mismatches 223; Indels 34; Gaps 11;  
Qy 6 LGAALLPLLAAYEETLMDSTTATAEIGWVHPGSGVEEVSVDENMTIRTYQVNCVF 65  
Db 46 LCAALRTLLASPSNEVLLDSRTVWGLGWIAFPNGWEEIGEVDENYAPHTYQVCKVM 105  
Qy 66 ESSQNNWLRTKPIRRGAHRIHVEMKFSVRDCSSIPVSGSKETFNLYYEADFDSATK 125  
Db 106 EQNNWLLTSWISNEGASRIFELKTLRDCNSLPGGLGTCETFNMYFESDDQNGR- 164  
Qy 126 TFPNWMENPVKVTIIADEFSDVLDLGRVKNLNTVEPSFGPVSRSGFYLAFOYGGCM 185  
Db 165 ---NIKENQYIKIDTIAADEFSDVLDLGRVKNLNTVEPSFGPVSRSGFYLAFOYGGCM 221  
Qy 186 SLIAVRVYRKPRIQNGAIFQETLSGABSTSLVAARGSCIANAEVDPVPIKLYCNGDG 245  
Db 222 ALVSRVYRKPRIQNGAIFQETLSGABSTSLVAARGSCIANAEVDPVPIKLYCNGDG 280  
Qy 246 EWLVPICMKCKAGFAEAVENGTCVCGPSGTFKANKQDEACTHCPINSRTTSEGATNCVC 305  
Db 281 EWLVPICMKCKAGFAEAVENGTCVCGPSGTFKANKQDEACTHCPINSRTTSEGATNCVC 338  
Qy 306 RNVYRADLPLDMPCTTIPSAQVITSSVNETSLMLEWTPPRDSGGREDLVNIIICKSC 365  
Db 306 RNVYRADLPLDMPCTTIPSAQVITSSVNETSLMLEWTPPRDSGGREDLVNIIICKSC 365

Db 339 EKDYFRSEDPPTMACTRPPSAPRNAISNVNETSVFLEWIPPADTGGKRVSYIACKKC 398  
Qy 366 GSGRGACTRCGDNVQVAPROLGLTEPRIYISDLIAHTQYTFEIOAVNGVTDQSPFPOFA 425  
Db 399 NSHAGVCEEGCHVRYLPQSGGLKNTSVMMVVDLLAHTNYTFEAVNGVSDLSFGARQYV 458  
Qy 426 SVNITTQAAAPSIVSMHQSRTVDSITLWSQDPQNGVILDYELQYKEKSEYNATA 485  
Db 459 SVNITTQAAAPSIVSMHQSRTVDSITLWSQDPQNGVILDYELQYKEKSEYNATA 517  
Qy 486 IKSPNTVTVQGLKAGAIYVQVRAVYAGYSGYSGMYFQMTAEAYQYSIOEKLPII 545  
Db 518 IKSPNTVTVQGLKAGAIYVQVRAVYAGYSGYSGMYFQMTAEAYQYSIOEKLPII 576  
Qy 546 GSSAAGLVFLIAVVAIV-----CNRR-----GPERADSEYTDKLOH 583  
Db 577 VSVTVGVILLAVVIGVLLSGCCGCCGRASSLCAVAHPILIWRCGYSKAQDPEEEKMH 636  
Qy 584 YTSGHM-TPQMKYIYDPFTVEDPNEAVREFAKEDIDSCVKEIQVIGAGEFGEVCSHLKL 642  
Db 637 FHNGHIKLPGRVTVYIDPHTYEDPNQAVHEFAKBIASCIITRIERVIGAGEFGEVCSHLKL 696  
Qy 643 PGKREIFVAIKLKSQYTERKORBDLSEASIMGOFDHPNVHLEGVVTKSTPVMITFEM 702  
Db 697 PGKREIFVAIKLKSQYTERKORBDLSEASIMGOFDHPNVHLEGVVTKSTPVMITFEM 756  
Qy 703 ENGLSDSFLRQNDGQFTVIQLVGMGLTAAAGKYLADNNYVHRDLAARNILVNSLVCKV 762  
Db 757 ENGLSDSFLRQNDGQFTVIQLVGMGLTAAAGKYLADNNYVHRDLAARNILVNSLVCKV 816  
Qy 763 SDFGLSRFLEDDTSDPTYSALGKIPIRWTAPEAIQYRKFTSASDVMSYGIVMVEVMSY 822  
Db 817 SDFGLSRFLEDDTSDPTYSALGKIPIRWTAPEAIQYRKFTSASDVMSYGIVMVEVMSY 874  
Qy 823 GERPYWDMNQDINAIQDDYRLPPMDCPSALHQLMDCQKORNRHPRKFGQIVNTLDK 882  
Db 875 GERPYWDMNQDINAIQDDYRLPPMDCPSALHQLMDCQKORNRHPRKFGQIVNTLDK 934  
Qy 883 MIRNPNLSKAMAPLSSGNLPDLRTIPDYSFNTVDEWLEAKMGQYKESFANAGFTSP 942  
Db 935 LIENPSSKLTVNASCRVSNLAEHSPGSGVSRSGFYLAFOYGGCM 994  
Qy 943 DVVSQMMEDILRLGVTLAGHKKILNLSQVMAQW 978  
Db 995 DAVAQVTLERLRLGVTLVGHQKIMNSLOEMKVL 1030

RESULT 22  
US-10-353-690-40  
; Sequence 40, Application US/10353690  
; Publication No. US20030215840A1  
; GENERAL INFORMATION:  
; APPLICANT: Logan, Thomas Joseph  
; APPLICANT: Chun, Miyoung  
; APPLICANT: Galvin, Katherine M.  
; APPLICANT: Healy, Aileen  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Donoghue, Mary  
; APPLICANT: Stagliano, Nancy  
; APPLICANT: Perodin, Jacquelin  
; APPLICANT: Rodrigue-Way, Amelie  
; TITLE OF INVENTION: Methods and compositions for treating  
; TITLE OF INVENTION: Cardiovascular disease using 1682, 6169, 6193, 7771, 14395,  
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 32427, 32427, 32427, 32427,  
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,  
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,  
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,  
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,  
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,  
; FILE REFERENCE: MP102-018P1RNMNM  
; CURRENT APPLICATION NUMBER: US/10/353,690  
; CURRENT FILING DATE: 2003-01-29



```
Qy 320 PCTTIPSAQAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCSGRGACTRCGDNV 379
Db 296 ACTRPPSAPRNAISNVNETSVFLEWIPADTGGKDKVSYIACKNCNHHAGVCECGHV 355
Qy 380 QYAPRQLGTEPRIYISDILAHQYTFEIOAVNGVTDQSPFOPASVNIITNQAAPSAV 439
Db 356 RYLPQROGLKNTVMYVDDLAHTNYTFEIBAVNGVSDLSFGARQYVSVNVTTNQAAESPV 415
Qy 440 SINHOVSRTVDSITLSWQDPQNGVILDEYVYKELSEYNATAIKSPNTNTVVOGLK 499
Db 416 TNVKGKIAKNSISLSWQEDRPNGLILEYKHFED-QETSVTIKSKETITABGLK 474
Qy 500 AGAIYFQVARTVAGYGRYKMYFOTMTEAEYQTSIQBKPLIIGSSAAGLVFLIYV 559
Db 475 PASVYVQIRARTAAAGYVFSRREFET-TPVFAASDQSIPIVAVSVTVGVILLAVI 533
Qy 560 VIAIV-----CNRR-----GPERADSEYTDKLOHYTSGHM-TPGKMIY 596
Db 534 GVLLSGSCCGGRASSLCAVAHPILIWRGYSKAKODPEEEKHHPHNGHKLPGVRTY 593
Qy 597 IDPTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLK 656
Db 594 IDPHYEDPNAVHEFAKEIEASCITIERVIGAGEFGEVCSGRLKLPKRELPAIKTLK 653
Qy 657 SGYTEKORRDFLSPASIMGQFDHPNVHLSEGVYKSTPVMIIITFMENGSLDPLRONDG 716
Db 654 VGYTEKORRDFLSEASIMGQFDHPNIIHLEGVYTKSKPVMIVTEYMEGSLDTPFKKNDG 713
Qy 717 QFTVIQVGLMGLGTAGMKVYLDAMNVYHRLAARNILVNSLVCKSDGLSRFLEDDTS 776
Db 714 QFTVIQVGLMGLGISAGMKYLSDMGYVHRLAARNILVNSLVCKSDGLSRVLEDD-P 772
Qy 777 DPTVTSALGKIPIRWTAPAIQVRKFTSADVMSYGIWVMEVMSYGERPYWDMNQDVI 836
Db 773 EAAVTR-GGKIPIRWTAPEAIAERKFTSADVMSYGIWVMEVMSYGERPYWETNQDVI 831
Qy 837 NAIEQDYLPPMDPCPSALHQLMLDCWQKORNRHPRKFGQIVNTLDKMRNPNSLKAWAPL 896
Db 832 KAVEGVRPLSPMDCPAALYQLMLDCWQKERNRPKFDIWNMLDKLIRNPSSLKLVNA 891
Qy 897 SSGINLPLDRTPDYTSFNTVDEWLEAIKWQYKESFANAGFTSPDVUSQMMEDILRL 956
Db 892 SCRVSNLLAHSPLGSGAYSVGWLEAIKWGRYTEIFMENGYSYMDAVAQVTLLELRL 951
Qy 957 GVTLAGHKKILNSIQVMRAQM 978
Db 952 GVTLVGHQKKIMNSLOEMKVQL 973

RESULT 24
US-09-823-187-40
; Sequence 40, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spaderna, Steven K
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier, Raymond J
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-745
; CURRENT APPLICATION NUMBER: US/09/823,187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/193,339
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/193,205
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/195,343
```

```
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,088
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,005
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,792
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/196,556
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/197,081
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/197,525
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/197,087
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-187-40

Query Match 58.4%; Score 3028; DB 10; Length 998;
Best Local Similarity 59.1%; Pred. No. 5.2e-191;
Matches 574; Conservative 153; Mismatches 224; Indels 20; Gaps 9;

Qy 17 AAVEETLMDSTTATAELGMMVHPSPGWEVSGYDENNTIRTYQVCNVFSSQNNWLRTK 76
Db 29 AAKEVLLDLSKAQOTLEWISSPPNGWEEISGLDENYTPRTYQVCQVMPNQNNWLRTN 88
Qy 77 FIRRGARHRIHVMEKFSVRDCSSIPSVPGSKETFNLYYEADPDSATKTFPNMNPWV 136
Db 89 WISGNAQRIFVELKFTLRDCNSLPGVLGTCETFNLYYETDYE----TGRNIRENLV 144
Qy 137 KVDTIAADESFQVDLGGVRVKNINTEVRSGFVSRSGFYLAFOYGGCMLIAVRVYRK 196
Db 145 KIDTIAADESFQVDLGGVRVKNINTEVRSGFVSRSGFYLAFOYGGCMLIAVRVYRK 204
Qy 197 CPRIIONGALFQBTLSGAESTLSVAARGSCIANA-BEVDVPIKLYCNGDGEWLVPICRM 255
Db 205 CWSIIEENLAIPTDVTGSEFSSILVEVRGTCVSSABEEAENAPRMHCSAGEWLVPICKI 264
Qy 256 CKAGFEAVENGTVCRGCPSTGTFKANQOGEACTHCIPINSRTTSEGATNCVCNRYRADLD 315
Db 265 CKAGYQ--QKGDTCPCGRCGRFYKSSQDLQCSRCPHSPSDKEGSSRCECEDGYRAPSD 322
Qy 316 PLDMPCTTTPSAQAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCSGRGACTRC 375
Db 323 PYYVACTRPPSAPQNLIFNINQTTVSLWSPPADNGGRNDVTYRILCKRCSWEQGEVPC 382
Qy 376 GDNVQYAPRQLGTEPRIYISDILAHQYTFEIOAVNGVTDQSPFOPASVNIITNQAA 435
Db 383 GSNIGYMPQOTGLEDNVYVMDLLAHANYTFEIVAVNGVSDLSRQSLFAVSLTTQAAA 442
Qy 436 PSASIMHQSRTVDSITLSWQDPQNGVILDEYVYKELSEYNATAIKSPNTNTVTV 495
Db 443 PSQVSGVMKERVLRQSVLSWQEPHPNGVITEYIKYEQDQRETRTYSTVTKTSTASI 502
Qy 496 QGLKAGAIYFQVARTVAGYGRYKMYFOTMTEA-----EYQTSIQEKLPLIGS--S 548
Db 503 NNLKPGTVYVQIRARTAAAGYVFSRREFET-TPVFAASDQSIPIVAVSVTVGVILLAVI 562
Qy 549 AAGLVFLIAVVVIAIVCNRR-GPERADSEYTDKLOHYTSGHMTPGMKIYIDPFTYEDPNE 607
Db 563 VAGTIIILVFMVFGFIIGRRHCGYSKADQEGDESLYFH---FKPGTYTIDPTEYEDPNR 619
Qy 608 AVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDF 667
Db 620 AVHQFAKELDASCIKIERVIGAGEFGEVCSGRLKLPKRDVAVAIKTLKVGYTEKORRDF 679
Qy 668 LSEASIMGQFDHPNVHLSEGVYKSTPVMIIITFMENGSLDPLRONDGQFTVIQVGLM 727
```

Db 680 LCEASIMGQFDHPNVHLEGVVTRGKPVNIVIEFMENGALDAFLRKHGQFTVIQVGM 739  
QY 728 RGIAAGMKYLDNMVYHRLAARNILVNSLVCKYSDFGLSFLEDDTSDPTYSALGK 787  
Db 740 RGIAAGMKYLDNMVYHRLAARNILVNSLVCKYSDFGLSFLEDDTSDPTYSALGK 797  
QY 788 IPIRWTAPAIQYRKFTSASDVMSYGIWVWVMSYGERPYDMTQDVINAIEODYRLPP 847  
Db 798 IPIRWTAPAIQYRKFTSASDVMSYGIWVWVMSYGERPYDMTQDVINAIEODYRLPP 857  
QY 848 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMKINRPNLSLKAWAPLSGINLPLDR 907  
Db 858 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMKINRPNLSLKAWAPLSGINLPLDR 917  
QY 908 TTPDYSFNTVDLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGLVTLACHOKKI 967  
Db 918 TTPDYSFNTVDLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGLVTLACHOKKI 977  
QY 968 LNSIQVMAQM 978  
Db 978 MSSIQVMAQM 988

## RESULT 25

US-09-823-187-42  
; Sequence 42, Application US/09823187  
; Publication No. US20030096952A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Gusev, Vladimir Y  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Majumdar, Kumud  
; APPLICANT: Padigaru, Muralidhar  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Taupier, Raymond J  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-745  
; CURRENT APPLICATION NUMBER: US/09/823,187  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/193,339  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/193,205  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/195,343  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: 60/195,088  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,005  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,792  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: 60/196,556  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: 60/197,081  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/197,525  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/197,087  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 103  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 998  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-823-187-42

Query Match 58.1%; Score 3013; DB 10; Length 998;  
Best Local Similarity 58.6%; Pred. No. 5.1e-190;  
Matches 572; Conservative 157; Mismatches 217; Indels 30; Gaps 11;

QY 17 AAVEETLMDSTTAAEAGVMVHPSPSGHEVEVSGVDENNNTIRTYQVCMVFESSQNNWLRTK 76  
Db 29 AAKEVLLDLSKAQOLETELEWISPPSGWEEISGLDENYTPRTYQVCMVFESSQNNWLRTN 88  
QY 77 FIRRGAGHRITHVEMKFSVRDCSSITPSVPGSKCTENLYYYEADFSDATKTFPNMNMW 136  
Db 89 WISKGNQRIPLVELKFTLRCNSLPGVLGTCETENLYYYETDYD---TGRNIRENLYV 144  
QY 137 KVDTIAADESFQSDVGLGRVMKINTEVRSFPGVSRSGFYLAFOYDYGCMSLIAVRVYFRK 196  
Db 145 KIDTIAADESFTQDGLGERKMKLNTVEIRGIPGLSKGFLYLAFOVDGACIALVSKVYKK 204  
QY 197 CPRIIIONGAIPOETLSGAESTSLVAARGSCIANA--BEVDVPIKLYCNGDGEWLVPTGRCM 255  
Db 205 CWTIVENLAFFDITVTSSEFSSLEVRGTCVSSAEEBAENSPRMHCSAGEWLVPTGKCI 264  
QY 256 CKAGFAVENGTVCRCGPGTGFKANOGDEACTHCPINSTRTSSEGTATNCVCRNGVYRADLD 315  
Db 265 CKAGYQ--QKGDTCPCGRRFYKSSQDLQSCRCPHSPDSRSGRCEGEGYIRAPSD 322  
QY 316 PLDMPCITTPSAPQAVISSVNETSLMELWTPPRDSGREDLVNIIICKSGSGRGCATRC 375  
Db 323 PYYVACTRTPSPAPQNLIFINQTTVSLWSPPADNGGRNDVTYRILCKRCSWEOGECVPC 382  
QY 376 GDNVQVAPRGLGTEPRIYISDLAHTOYTERIQAVNGVTDQSPSPQFASNITTNOA 435  
Db 383 GSNIGVWPOQTGLEDNVYVMDLAAHANTFEVAVNGVSDLSRSORLFAAVSITGQAA 442  
QY 436 PSAVIMHQRVTRVDSITLSWSQPDOPNGVILDYLOYYEKELSEYNATAIKSPNTTVTV 495  
Db 443 PSQVSGVMKERVLRQSVQLSWQEPHPNGVITEYEIKYKQQRERTYTLTKTSASAI 502  
QY 496 QGLKAGAIYVQVRARTVAGYGRYKMYFQNTWEA-----EYQTSIQEKLPLITGS--S 548  
Db 503 NNLKPGTVYVQIRAVTAAGYGNYSPLDVATLEASGRMFEATAVSSSQNPVILIAVVA 562  
QY 549 AAGLFLIAVVAIAIVCNR--GFERADSEYTDKLOHYTSCMTGPMKIYIDPFTVEDPNE 607  
Db 563 VAGTILVFMVFGFIIGRHCYKADQSGDELFH---FKFPGTKYIDETVEDPNE 619  
QY 608 AVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDF 667  
Db 620 AVHQFAKELDASCIKIERVIGAGEFGEVCSGRLKLPQORDVAIVAKTLKVGYTEKORRDF 679  
QY 668 LSEASIMGQFDHPNVHLEGVVTRKPVMIITEFMENGSLDSFLRQNDGQFTVIQVGM 727  
Db 680 LCEASIMGQFDHPNVHLEGVVTRKPVMIITEFMENGALDAFLRKHGQFTVIQVGM 739  
QY 728 RGIAAGMKYLDNMVYHRLAARNILVNSLVCKYSDFGLSFLEDDTSDPTYSALGK 787  
Db 740 RGIAAGMKYLDNMVYHRLAARNILVNSLVCKYSDFGLSFLEDDTSDPTYSALGK 797  
QY 788 IPIRWTAPAIQYRKFTSASDVMSYGIWVWVMSYGERPYDMTQDVINAIEODYRLPP 847  
Db 798 IPIRWTAPAIQYRKFTSASDVMSYGIWVWVMSYGERPYDMTQDVINAIEODYRLPP 857  
QY 848 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMKINRPNLSLKAWAPLSGINL 902  
Db 858 PMDCPSALHQLMDCWQKDRNHRPKFGQIVNTLDMKINRPNLSLKAWAPLSGINL 912  
QY 903 PLLDRTIDPYSFNTVDLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGLVTLACHOKKI 962  
Db 913 PLLDRTIDPYSFNTVDLEAIKMGQYKESFANAGFTSFVVSQMMEDILRLGLVTLACHOKKI 972  
QY 963 HOKKILNSIQVMAQM 978  
Db 973 HOKKILNSIQVMAQM 988

RESULT 26  
US-09-823-187-43  
; Sequence 43, Application US/09823187



```
Db 29 EVNLLDSKTIQBELGWSYPSHGWEISGVDEHYPIRTYQVCNVMDSQNNWLTNNVP 88
Qy 80 RRGARHIVHEMFESVDCSSIPSVCSEKTNLYYYEADFSAKTTPNNMENPWKVD 139
Db 89 RNSAQKIYVELKFTLRDCNSIPLVGTCKETNLYYMSDDDHGVK---FREHQTID 144
Qy 140 TIAADESFQVDLGGRWKINTEVRSFGVSVSGFVLAPODYGGCMSLIAVRFVKCPR 199
Db 145 TIAADESFQMDLGRILKLANTEIREVGVNKGFFLAPODVGACVALSVRVYKPCPF 204
Qy 200 ITONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPTIGRCWKAG 259
Db 205 TVKNLAMPDTPV-MDSQSLVEVRGSCVNSKEEDPP-RMYCSTEGEWLPIGKSCNAG 262
Qy 260 FBAVNGTVCRCPGSGTFCANQGDDEACTHCPINSETTSEGATNCVCRNGYVRADLDPLDM 319
Db 263 YE--ERGFMCQACRFGFKALDGNMKCAKCPHSSSTQEDGSMNRCENNYFRADKPPSM 320
Qy 320 PCTTIPSAQVAISSVNETSLMLEWTPPRDSGREDLVYNIICKSGSGRGACTRCGDNV 379
Db 321 ACTRPPSSPRNVISINETSVIDLWSWPLDTGGRKDVTFNIIKCKGNWIKQCEPCSPNV 380
Qy 380 QYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPSPOPASVNIITNQAAPSAV 439
Db 381 RELPRQFGLTNTVTVDLLAHTNTYTFEIDAVNGVSELSPRPQFAAVSIITNQAAPSPV 440
Qy 440 SIMHQVSRVDSITLSWSQOPQNGVILDYEQYKEKSELYNATAIKSPNTVTVOGLK 499
Db 441 LTIKORTSRNISLSWQEPHPNGIILDYEVKYEQEQTSTYILNARTNTVITISL 500
Qy 500 AGAIYVFOVRARTVAGYGRYSGKMYFOTMTEAEYQTSIQEKLPLIIGSSAAGLVFLIAV 559
Db 501 PDTIYVFOIRARTAGYGRYSGKMYFOTMTEAEYQTSIQEKLPLIIGSSAAGLVFLIAV 559
Qy 560 VIAIV---CNRRGPERADSEYTKLQHYTSCHM-TPGMKIYIDPFTVEDPNEAVREPAKE 615
Db 560 IYVLIGFCGYKXHGAD---EKRLHFGNHLKLPGLRTYVDHTYEDPTQAVHEPAKE 615
Qy 616 IDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDRFLSEASIMG 675
Db 616 LDATNISDKVVGAGEFGEVCSGRLKLPKSEISVAIKTLKGVYTEKQRDRFLGEASIMG 675
Qy 676 QFDHENVHLRGVUTKSTPVMIIITFPMENGLDSFLRQNDQOFTVIOLVGMRLGIAAGMK 735
Db 676 QFDHENVIRLEGVVTKSPVMIVTEYMEENGSLDSFLRKHDAQFTVIOLVGMRLGIAAGMK 735
Qy 736 YLADNMYVHRDLAARNILVNSNLVKYSDFGSLRFLDDTSDPTYTSGALGKPIRWTAP 795
Db 736 YLSDMGVYHRDLAARNILVNSNLVKYSDFGSLRFLDD-PEAYITR-GGKPIRWTSP 793
Qy 796 EAIQYRKFTSASDVMSYGIVMWEVMSYGERPYWDMTNDQVINAEQDYRLPPPMDCPSAL 855
Db 794 EAIYRKFTSASDVMSYGIVLWEVMSYGERPYWEMSNQDVIKAVDEGYRLPPPMDCPSAL 853
Qy 856 HOLMDCQKDRNRHPRFGQIVNTLDKMIENPNSLKAAPLSSGINLPLDRIPIDYSF 915
Db 854 YQLMDCQKDRNRHPRFQIVNTLDKMIENPNSLKAAPLSSGINLPLDRIPIDYSF 913
Qy 916 NTVDWELEAKMGQYKESFANAGFTSPDVVSQMMEDILRLGVLTAHQKILNLSIQVMR 975
Db 914 RTTGDLNGVTRACHKEIFTGVEYSCDTIAKISTDDMKKVGVTVVGPQKKIISIKALE 973
Qy 976 AQ 977
Db 974 TQ 975
```

RESULT 28

US-10-205-823-97

; Sequence 97, Application US/10205823

; Publication No. US20030108963A1

; GENERAL INFORMATION:

```
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Deede, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kanatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MKI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-97
```

Query Match 56.5%; Score 2930.5; DB 14; Length 983;

Best Local Similarity 57.0%; Pred. No. 1.4e-184;

Matches 548; Conservative 172; Mismatches 223; Indels 19; Gaps 10;

```
Qy 20 EETLMDSTTATLGMVHPSPSGWEVSGYDENMTIRTQVCNVPFESSONWLTNVP 79
Db 29 EVNLLDSKTIQBELGWSYPSHGWEISGVDEHYPIRTYQVCNVMDSQNNWLTNNVP 88
Qy 80 RRGARHIVHEMFESVDCSSIPSVCSEKTNLYYYEADFSAKTTPNNMENPWKVD 139
Db 89 RNSAQKIYVELKFTLRDCNSIPLVGTCKETNLYYMSDDDHGVK---FREHQTID 144
Qy 140 TIAADESFQVDLGGRWKINTEVRSFGVSVSGFVLAPODYGGCMSLIAVRFVKCPR 199
Db 145 TIAADESFQMDLGRILKLANTEIREVGVNKGFFLAPODVGACVALSVRVYKPCPF 204
Qy 200 ITONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPTIGRCWKAG 259
Db 205 TVKNLAMPDTPV-MDSQSLVEVRGSCVNSKEEDPP-RMYCSTEGEWLPIGKSCNAG 262
Qy 260 FBAVNGTVCRCPGSGTFCANQGDDEACTHCPINSETTSEGATNCVCRNGYVRADLDPLDM 319
Db 263 YE--ERGFMCQACRFGFKALDGNMKCAKCPHSSSTQEDGSMNRCENNYFRADKPPSM 320
Qy 320 PCTTIPSAQVAISSVNETSLMLEWTPPRDSGREDLVYNIICKSGSGRGACTRCGDNV 379
Db 321 ACTRPPSSPRNVISINETSVIDLWSWPLDTGGRKDVTFNIIKCKGNWIKQCEPCSPNV 380
Qy 380 QYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPSPOPASVNIITNQAAPSAV 439
Db 381 RELPRQFGLTNTVTVDLLAHTNTYTFEIDAVNGVSELSPRPQFAAVSIITNQAAPSPV 440
Qy 440 SIMHQVSRVDSITLSWSQOPQNGVILDYEQYKEKSELYNATAIKSPNTVTVOGLK 499
Db 441 LTIKORTSRNISLSWQEPHPNGIILDYEVKYEQEQTSTYILNARTNTVITISL 500
Qy 500 AGAIYVFOVRARTVAGYGRYSGKMYFOTMTEAEYQTSIQEKLPLIIGSSAAGLVFLIAV 559
```

```
Db 501 PDIYVQIARATAGTNSRKPEFETSPDS-FSISGESSQVVMIAISAVALITTV 559
Qy 560 VIAIV---CNRRGPERADSEYTKLOHYTSGHM-TPGMKIYIDPFTYEDPNEAVEPAKE 615
Db 560 IYVLIGFCGYKSKHGAD---EKRLHFGNHLKLPGLRTYVDPTVEDPTQAVHEPAKE 615
Qy 616 IDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKLKGYTEKQRDFLSEASIMG 675
Db 616 LDATNISIDKVGAGEFGEVCSGRLKLPKSKEISVAIKLKGYTEKQRDFLSEASIMG 675
Qy 676 QFDHPNVHLEGVVTKSTPWMIITEFMENGLSDFLRNDGQFTVIOVLGMLGIAAGMK 735
Db 676 QFDHPNIIIRLEGVVTKSKPMVIITEFMENGLSDFLRNDGQFTVIOVLGMLGIAAGMK 735
Qy 736 YLADMYVHRDLAARNILNSNLVKVDFGLSRFLEDDTSDPTTYSALGKPIRWTPAP 795
Db 736 YLSDMGVYHRDLAARNILNSNLVKVDFGLSRFLEDD-PEAAYTTR-GGKPIRWTPSP 793
Qy 796 EAIQYRKFTSASDWSYGIWMEVMSYGERPYDMTQDVINAIEQYRLPPPMDCPSAL 855
Db 794 EAIAYRKFTSASDWSYGIWMEVMSYGERPYDMTQDVINAIEQYRLPPPMDCPSAL 853
Qy 856 HOLMDCWQDRNHRPKFGQIVNTLDKMIIRNPNSLKAWPLSSGINPLDRTIPDYTSF 915
Db 854 YQLMDCWQDRNHRPKFGQIVNTLDKMIIRNPNSLKAWPLSSGINPLDRTIPDYTSF 913
Qy 916 NTVDWELEAIKMGQYKESFANAGTSPDVVVSQMMEDILRLGVTLAGHQKILNSIQVMR 975
Db 914 RTTGDWLVNGVYRTAHCKEIFTGVEYSSCDTAKISTDDMKKGVTVVGPQKKIISIKALE 973
Qy 976 AQ 977
Db 974 TQ 975

RESULT 29
US-10-345-680-2
; Sequence 2, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323.
; TITLE OF INVENTION: 12303, 985, 12237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: ME102-012P1RNM OMNI
; CURRENT APPLICATION NUMBER: US/10345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 983
; TYPE: PRT
```

```
; ORGANISM: Homo Sapiens
US-10-345-680-2
Query Match 56.5%; Score 2930.5; DB 14; Length 983;
Best Local Similarity 57.0%; Pred. No. 1.4e-184;
Matches 548; Conservative 172; Mismatches 223; Indels 19; Gaps 10;

Qy 20 EETLMDSTTATABELGMVHPSPSGWEEVSGYDENMTIRTYQVCNVFESSQNNLRTKPIR 79
Db 29 EVNLLDSKTIQELGELGWSYPSHGWEEISGVDEHYTPITRTYQVCNVMDHSQNNLRTNWVP 88
Qy 80 RRGARHIVHMKSVSDCSSIPSPGSKETFNLYYYEADFDSATKTFFPMWENPWTXVD 139
Db 89 RNAQAQIYYVELKFTLRLDCNSIPLVLTGKTFNLYYMESDDDHGVK----FREHQFTKID 144
Qy 140 TIAADSFSDVLDGGVGMKINTEVRSGFVPSRSGFLAFODYDGGCNSLIARVVFYRKCPR 199
Db 145 TIAADSFSTQMDLGRILKILNTEIREVGPVKNKGFLAFODVACALVSVRVYFKCPCF 204
Qy 200 IIQNGAIFQBTLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRMCCKAG 259
Db 205 TVKNLAMPDTPV-MDSQSLVEVRGSCVNSKEEDPP-RMYCSTEGEWLVPIGRKCSNAG 262
Qy 260 FEAVENGTVCRGCPSTGTFKANQDDEACTHCPINSRTTSEGATNCVCGNGYTRADLDPLDM 319
Db 263 YE--ERGFMCQACRPGFYKALDGNMKCAKCPHPSSTQEDGSMNCRCCENNYFRADKDPSPM 320
Qy 320 PCTTIPSAQAVTSVSNVETSLMEWTTPRDSGREDLVNIIICKSGSGRGACTRCCGDNV 379
Db 321 ACTRPSSPRNVLSNINETSVIDLWSWPLDTGKGVTFNIIICKCGWNTKQCEPCSPNV 380
Qy 380 QYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOAAPSVA 439
Db 381 RFLPRQFGLTNTVTVDLLAHTNYTFEIDAVNGVSELSPPRQFAAVSITTNQAAPSPV 440
Qy 440 SIMHVSRTVDSITLSWSPDQPNQVILDYELQYKELSEYNATAIKSTNTVTVOGLK 499
Db 441 LTIKDORTSRNSISLSWQEPHNGIILDEYEVYKQEQTSTYTLRAEGTNTVTSLSK 500
Qy 500 AGAIYVFOVRAITVAGVGRYSGWYFOTMTEAEVQTSIOEKLPLIIGSSAAGLVFLAVV 559
Db 501 PDIYVQIARATAGTNSRKPEFETSPDS-FSISGESSQVVMIAISAVALITTV 559
Qy 560 VIAIV---CNRRGPERADSEYTKLOHYTSGHM-TPGMKIYIDPFTYEDPNEAVEPAKE 615
Db 560 IYVLIGFCGYKSKHGAD---EKRLHFGNHLKLPGLRTYVDPTVEDPTQAVHEPAKE 615
Qy 616 IDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKLKGYTEKQRDFLSEASIMG 675
Db 616 LDATNISIDKVGAGEFGEVCSGRLKLPKSKEISVAIKLKGYTEKQRDFLSEASIMG 675
Qy 676 QFDHPNVHLEGVVTKSTPWMIITEFMENGLSDFLRNDGQFTVIOVLGMLGIAAGMK 735
Db 676 QFDHPNIIIRLEGVVTKSKPMVIITEFMENGLSDFLRNDGQFTVIOVLGMLGIAAGMK 735
Qy 736 YLADMYVHRDLAARNILNSNLVKVDFGLSRFLEDDTSDPTTYSALGKPIRWTPAP 795
Db 736 YLSDMGVYHRDLAARNILNSNLVKVDFGLSRFLEDD-PEAAYTTR-GGKPIRWTPSP 793
Qy 796 EAIQYRKFTSASDWSYGIWMEVMSYGERPYDMTQDVINAIEQYRLPPPMDCPSAL 855
Db 794 EAIAYRKFTSASDWSYGIWMEVMSYGERPYDMTQDVINAIEQYRLPPPMDCPSAL 853
Qy 856 HOLMDCWQDRNHRPKFGQIVNTLDKMIIRNPNSLKAWPLSSGINPLDRTIPDYTSF 915
Db 854 YQLMDCWQDRNHRPKFGQIVNTLDKMIIRNPNSLKAWPLSSGINPLDRTIPDYTSF 913
Qy 916 NTVDWELEAIKMGQYKESFANAGTSPDVVVSQMMEDILRLGVTLAGHQKILNSIQVMR 975
Db 914 RTTGDWLVNGVYRTAHCKEIFTGVEYSSCDTAKISTDDMKKGVTVVGPQKKIISIKALE 973
Qy 976 AQ 977
```

```

Db          974 TQ 975

RESULT 30
US-10-295-027-602
; Sequence 602, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 016501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 602
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-602

Query Match          56.5%; Score 2930.5; DB 14; Length 983;
Best Local Similarity 57.0%; Pred. No. 1.4e-184;
Matches 548; Conservative 172; Mismatches 223; Indels 19; Gaps 10;

Qy          20  EETLMDSTTAAELGVMVHPSPGVEEYSGVDENNMTIRTYQVCNVFSSQNNMLRTKFR 79
Db          29  EVNLLDSTKIQELGWSYPSHGHEEISGVDEHYPTIRTYQVCNVMDHSQNNMLRTNWVP 88

Qy          80  RRGHRIHVMKFSVRDCSSIPSPVSGSKETFNLYYEADFDSATKTFPNMNMNPNWKVD 139
Db          89  RNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDHGK----FREHQFTKID 144

Qy          140  TIAADESFQVDLGRGVKINTEVRSFQVSRSGFYLAFOGYGCMSLIAVRVYRKCPR 199
Db          145  TIAADESFTQMDLGRILKUNTEIREVGPVNKGFLAFQDVGACVALSVRVYFKCPE 204

Qy          200  IIONGALFOETLSGAESTSLVAARGSCIANAEVVDVPIKLYCNGDGEWLVPICRMCCKAG 259
Db          205  TVKULAMFPDTPV-MDSQSLVEVRGSCVNNKEDPP-RMYCSTEGEWLVPICKSCNAG 262

Qy          260  FEAVENGTVCRGCPSGFTFKANQDGEACTHCPINSRTTSEGATNCVCRNGYRADLDPLDM 319

```

Search completed: December 30, 2004, 16:54:18  
Job time : 166 secs

```

Db          263  YE--ERGFMCQACRPGFYKALDGNMKCAKPPSSSTQEDGSMRCRCENNYFRADKDPSPM 320
Qy          320  PCTTIPSAQAVISSVNETSLMLEWTPPRDGGREDLVYNIICKSCGSGRGACTRCGDNV 379
Db          321  ACTRPPSSPRNVISNETSVILDSWPLDTGGRKDVTFNIICKCGWNICKQCEPCSPNV 380
Qy          380  QYAPRQLGLTEPRIIYISDILLAHTQYTFEIOAVNGVTDQSPFQFASVNTTNOAAPS 439
Db          381  RFLPRQGLTNTTIVTDLAHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPV 440
Qy          440  SIMHOVSRTVDSITLSWQDPNGVILDYELQYKEKELSEYNATAIKSPNTNTVVGGLK 499
Db          441  LTIKORTSRNSISLSWQEPHENGILDEYKYEKQEQETSYTILRAGTNTVTSLLK 500
Qy          500  AGAIYVQVARTVAGRYSGKMYFQTMTEABYQTSIQEKLPIIIGSSAAGLVLI 559
Db          501  PDTIYVQIRARTAAAGYTNRSRKFETSPDS-FSISGESSQVVMIAISAVALILLTV 559
Qy          560  VIAIV---CNRGFERADSEYTDKLOHYTSGH-TFGMKIYIDPFTYEDNEAVRFAKE 615
Db          560  IYVLIGRFCGYKSKHGAD---EKRLHFGNGHLKLPGLRTYVDPHTYEDPTQAVHFAKE 615
Qy          616  IDISCVKIEOVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDFLSEASIM 675
Db          616  LDATNISIDKVGAGFGEVCSGRLKLPKSKELSAIKTLKVGYTEKQRDFLGEASIM 675
Qy          676  QPDHNVHLLEGVVTSTPMTIETPMENGSLDSFLRQNDGQPTVQLVGMRLGIAAGMK 735
Db          676  QFDHPNIIIRLEGVVTSTKPMIVTEYMWENGSLDSFLRKHDAQFTVQLVGMRLGIAAGMK 735
Qy          736  YLADMYVHRDLAARNILVNSNLVCKVSDPGLSRFLEDDTSDPTYSALGGKPIBWTAP 795
Db          736  YLSDMGVYHRDLAARNILVNSNLVCKVSDPGLSRVLEDD-PEAAYTTR-GGKPIBWTSP 793
Qy          796  EAIQYRKFTSASDVWSYGIWMEVMSYGRPYWDMTNQDVINAIEQDYRLPPPMDCPSAL 855
Db          794  EAIAYRKFTSASDVWSYGIWMEVMSYGRPYWMSNQDVIKAVDESGYRLPPPMDCPAL 853
Qy          856  HOLMLDCWQKDRNHRPKFGQIVNTLDKMTNPNLSKAMAPLSSGINLPILDRTPYTSF 915
Db          854  YQLMLDCWQKDRNHRPKFGQIVSILDKLIRNPGSLKIITSAARPSNLLDQSNVDISTF 913
Qy          916  NTVDLEWLEAIKMGQYKESFANAGTFSFVVSOMMEDILRLGYTLAGHOKKILNSIQVMR 975
Db          914  RTTGDWLVNGVTRTAHCKEIFTGVEYSCDTIAKISTDDMKKGVTVVGPQKKLISSIKALE 973
Qy          976  AQ 977
Db          974  TQ 975

```